

**From:** Hamud, Fozia  
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Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

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Searcher: \_\_\_\_\_  
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Date Picked Up: 5/6  
Date Completed: 5/13  
Searcher Prep/Review: 12  
Clerical: \_\_\_\_\_  
Online time: 12

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: g  
WWW/Internet: g  
Other (specify): \_\_\_\_\_

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 10:35:27 ; Search time 357 Seconds

(without alignments)  
15032.246 Million cell updates/sec

Title: US-09-912-157-1

Perfect score: 2383

Sequence:

1 ccgcgcgcgcacccacccac.....agcattgcacatttagctg 2383

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB-seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2383	100.0	2383	24	ABA95031	Human cytokine rec
2	2376.6	99.7	2383	24	ABA95033	Human cytokine rec
3	2289	96.1	2341	24	ABA95035	Human cytokine rec
4	2218.6	93.1	2786	24	AA518134	Human DNAX cytokin
5	2215.4	93.0	3083	23	AA515346	DNA encoding human
6	2158.4	90.6	4392	24	AA562082	Human cDNA encodin
7	2074.2	87.0	2319	22	AA509517	Human cDNA encodin
8	1638.4	68.8	2443	24	ABA95037	Murine cytokine re
9	1614.4	67.7	2259	24	ABA95032	Human cytokine rec

10	1612	67.6	2259	24	ABA95034	Human cytokine rec
11	1532	64.3	2217	24	ABA95036	Human zcytor18 spl
12	1496	62.8	2214	24	AA518135	Human DCR88 revers
13	1322.4	55.5	2217	24	ABA95038	Murine cytokine re
14	737.8	31.0	960	23	AA516201	5' portion of Huma
15	71.4	3.0	3223	17	AAT33801	Human interleukin-
16	71.4	3.0	3223	19	AAV27592	Human interleukin-
17	71.4	3.0	3223	20	AAV27592	Human IL-17R cDNA
18	71.4	3.0	3223	21	AA61240	Human IL-17R cDNA
19	71.4	3.0	3223	21	AA51988	Human interleukin-
20	71.4	3.0	3223	21	AA52146	Human interleukin-
21	71.4	3.0	3223	21	AA59871	Human interleukin-
22	71.4	3.0	3223	22	AA52815	Human interleukin-
23	71.4	3.0	3223	22	AA57188	Human IL-17R (RCTL
24	54.6	2.3	3288	17	AAT33800	Murine interleukin
25	54.6	2.3	3288	19	AAV27591	Murine interleukin-
26	54.6	2.3	3288	20	AA501921	Murine IL-17R cDNA
27	54.6	2.3	3288	21	AA61238	Murine interleukin
28	54.6	2.3	3288	21	AA51987	Murine interleukin
29	54.6	2.3	3288	21	AA52145	Murine interleukin
30	54.6	2.3	3288	21	AA59870	Murine interleukin
31	54.6	2.3	3288	22	AA502813	Murine interleukin
32	54.6	2.3	3288	22	AA57186	Murine IL-17R poly
33	49.6	2.1	1145	20	AA599114	Human cancer cell
34	49.2	2.1	1968	24	ABK10669	Human Epha truncat
35	49.2	2.1	2112	24	ABK10670	Human Epha extende
36	49.2	2.1	2955	24	ABK10667	Human Epha full le
37	49.2	2.1	3003	22	ABA01982	Human NOV3 coding
38	49.2	2.1	3099	24	ABK10668	Human Epha extende
39	49.2	2.1	114955	20	AA53491	Human adenosine A1
40	43.6	1.8	109519	22	AA508693	Micromonospora DNA
41	42.6	1.8	438	22	AAK75370	Human immune/hema
42	42.6	1.8	6125	22	AAK72745	Human cervical cau
43	42.6	1.8	6242	21	AA599495	Human cDNA encodin
44	42.2	1.7	9234	22	AAK89255	Human digestive sy
45	41.6	1.7	691	22	ABQ40810	Oligonucleotide fo

#### ALIGNMENTS

RESULT 1

ABA95031  
ID ABA95031 standard; DNA: 2383 BP.

AC ABA95031;

XX 20-MAY-2002 (first entry)

DE Human cytokine receptor, zcytor18 nucleotide sequence.

XX Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 86..2347

FT /tag- a

FT /product- "zcytor18"

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23253.

XX 26-JUL-2000; 2000US-220747P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;







QY	541	TAGCTTCAAAGAACTCGAATGGAATCTCAACCTTCTCTGTAATATGAATTTGAAACGGA	600
DB	541		600
QY	601	TTATTTCTGAAGGTGTCCCTTTCTTCTTCATTAAAAACGAAAGCAATTAACCACTTTT	660
DB	601		660
QY	661	CTTCTTTAGAACCGGAGCTGTGACCTGTGTTTACAGCGGAGCAATCTAGCTTGTAAACC	720
DB	661		720
QY	721	CTTCTGAAAGCTCGGAACCTGACATCAGCAGCATGCTCTGCATCATGACGTCTCCTT	780
DB	721		780
QY	781	CGACCATGCGGACGACAGCTTGGCTTCGGTTCTTCTATCTTCACTACAGCTCAAGCA	840
DB	781		840
QY	841	CGAAGGACCTTTCAAGCGAAAGACCTGTAAAGCAGGAGCAAACTACAGAGACACAGCTG	900
DB	841		900
QY	901	CCTCCTTCAAAATGTTTCTCCAGGGGATTATATAATTGAGCTGTTGGATGACACTAACAC	960
DB	901		960
QY	961	ARCACAAAGGTGATGCATTATGCTTTAAAGCAGTGACCTCCCGTGGCGCGGCCCAT	1020
DB	961		1020
QY	1021	CAGAGCGTGGGCAATCACAGTGCACCTGGTAGTCTATCGGCATTCGGCAGCTCTTCCAC	1080
DB	1021		1080
QY	1081	TGTGATGTGCGCGCAAGAGCAACAAGAAAAATATATTTCAATTTAGATGAAGAGAGCTC	1140
DB	1081		1140
QY	1141	TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGTCCTCGCGCGCGCGGAAGT	1200
DB	1141		1200
QY	1201	CTTTCTCTCTATTTCAGTAAAGATGGCCAGAAATCACATGAATCTGCTCCAGTGTTCGC	1260
DB	1201		1260
QY	1261	CTACTTCTCCAGACTCTGTGGCTGTGAGTGGCTCTGCACTCTGGAGAGACTTCAG	1320
DB	1261		1320
QY	1321	CCTCTGTAGAGAGGGCAGAGAAATGGGTCATCCAGAAGATCCAGAGTCCCAAGTTCAT	1380
DB	1321		1380
QY	1381	CATTGTGTGTTTGTCCAAAGGATGAAGTACTTTGTGGACAAGAGAACTACAAACACAA	1440
DB	1381		1440
QY	1441	AGGAGTGGCGGAGCTCGGGGAAAGGAGAGCTCTTCTGTGTGGCGGTGTACAGCATTCG	1500
DB	1441		1500
QY	1501	CGAAAGCTCCGACGCCACAGAGTGTGTCGGCGGCTCAGCAAGTGTATTCCGCGT	1560
DB	1501		1560
QY	1561	CTACTTTGATTATTTCTTGGGAGGAGAGCTCCCGGTATCTCTAGACCTGAGTACCAAGTA	1620
DB	1561		1620

1621	QY	CAGACTCATGGACAATCTTCCTCAGCTCTGTTCGCATCTGGACTCCGGAGACAGCGCT	1680
1621	Db	CAGACTCATGGACAATCTTCCTCAGCTCTGTTCGCATCTGGACTCCGGAGACAGCGCT	1680
1681	QY	CCAGGAGCCGGGCAGCACACGCGACAGGGCAGCAGAGGAMACTACTTCCGGAGCAATC	1740
1681	Db	CCAGGAGCCGGGCAGCACACGCGACAGGGCAGCAGAGGAMACTACTTCCGGAGCAATC	1740
1741	QY	AGGCCGGTCCCTCTATACGTCCCATTTGCAACATGCACCACTGTTTATTCAGCAGGAGCCCGA	1800
1741	Db	AGGCCGGTCCCTCTATACGTCCCATTTGCAACATGCACCACTGTTTATTCAGCAGGAGCCCGA	1800
1801	QY	CTGGTTGCAAAAGCAGTTTCGTTCCCTTCATCTCTCCCATCGCTACCGGGAGCCAGT	1860
1801	Db	CTGGTTGCAAAAGCAGTTTCGTTCCCTTCATCTCTCCCATCGCTACCGGGAGCCAGT	1860
1861	QY	CTTCGGAGAAATTTGATTCGGGCTTGTTTAAATGATGATCATGTGCAAACAGGCGCTGA	1920
1861	Db	CTTCGGAGAAATTTGATTCGGGCTTGTTTAAATGATGATCATGTGCAAACAGGCGCTGA	1920
1921	QY	GAGTGACTTCTGCCTAAAGGTAGAGCGGCTGTGTTTGTGGGCAACCGGACAGCGCACTC	1980
1921	Db	GAGTGACTTCTGCCTAAAGGTAGAGCGGCTGTGTTTGTGGGCAACCGGACAGCGCACTC	1980
1981	QY	CCAGCAGCAGAGATCAGCATGGGGCCCTGGACCAAGACGGGAGGCGCGGCTTGCCTTGA	2040
1981	Db	CCAGCAGCAGAGATCAGCATGGGGCCCTGGACCAAGACGGGAGGCGCGGCTTGCCTTGA	2040
2041	QY	CGTGTAGCGCGCCCTGCACACCCCTGCTGCACACGGTGAAGACGGCGACGCCCTCGGACAT	2100
2041	Db	CGTGTAGCGCGCCCTGCACACCCCTGCTGCACACGGTGAAGACGGCGACGCCCTCGGACAT	2100
2101	QY	CCGCGGGGACTCAGGCATCTATGACTCTGTCTGTGCGCCCTCATCCGAGCTGTCTTGCACAT	2160
2101	Db	CCGCGGGGACTCAGGCATCTATGACTCTGTCTGTGCGCCCTCATCCGAGCTGTCTTGCACAT	2160
2161	QY	GATGGAAAGACTCTCGACGACACAGCAAAAGCTCTTCCTTGAGGAGAGGCTGTCTC	2220
2161	Db	GATGGAAAGACTCTCGACGACACAGCAAAAGCTCTTCCTTGAGGAGAGGCTGTCTC	2220
2221	QY	CTCTCAGGCGTGGGTGAGGAGCACTCTCTGCGCCCTTCCTCCAAAGCTCTCTCTCTCG	2280
2221	Db	CTCTCAGGCGTGGGTGAGGAGCACTCTCTGCGCCCTTCCTCCAAAGCTCTCTCTCTCG	2280
2281	QY	GTCAATGCAAGCAGATCTTGTTTGGCGCAGCTACTGATGAATCCACCGCGTGCGCC	2340
2281	Db	GTCAATGCAAGCAGATCTTGTTTGGCGCAGCTACTGATGAATCCACCGCGTGCGCC	2340
2341	QY	TTTGTACAAAACGAAGAGTCTTAAGCATTCGCCACTTTAGCTG	2383
2341	Db	TTTGTACAAAACGAAGAGTCTTAAGCATTCGCCACTTTAGCTG	2383

**РЕСПУБЛИКА**

RESULT 3  
AB895035

ABA95035  
ID ABA95035 standard: DNA: 2341 BP.

XX  
AC  
AB795035.

XX: 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 splice variant nucleotide sequence.

XX  
XX

KW cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;

KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.  
 KW pulmonary alveolar proteinosis; familial pericardial effusion; antithrombotic;  
 KW

xx  
os Homo sapiens.

XX.	Key	Location/Qualifiers
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100	100	100

FT	key
ET	CDS

### III

FT . . . /product= "zcytor18 splice variant"





329	DB	CTTGCCATGCAAGATGGCAGTCCACATCTCTTTGGTCCCCAGGGGGCCCTCGCGCATCGAAT	388
447	QY	TCCTGAAGGATTTCCGGTAATACTATGGAGAGCTGAAGTCGGAGGGAAGACAGTCGCCAAC	506
389	DB	TCCTGAAGGATTTTCGGGTAATACTATGGAGAGCTGAAGTCGGAGGGAAGACAGTCGCCAAC	448
507	QY	AACCTGATTCATAAGGATCCGGAAGCAGCTCAACACAGTACGCTTCACAAAGAACTCGAATGGAAT	566
449	DB	AACCTGATTCATAAGGATCCGGAAGCAGCTCAACACAGTACGCTTCACAAAGAACTCGAATGGAAT	508
567	QY	CTCACCTTTCTCTGAATATGAATTTGAACGGATATTTCGTAAAGGTGTGCTTCCTTC	626
509	DB	CTCACCTTTCTCTGAATATGAATTTGAACGGATATTTCGTAAAGGTGTGCTTCCTTC	565
627	QY	CTTCCATATAAAGCAAGCAATACACACCTCTCTCTCTAGAACCCGAGCCTGTACC	686
566	DB	CCTTCATATAAAGCAAGCAATACACACCTCTCTCTTAGAACCCGAGCCTGTACC	625
687	QY	TGTTGTTACGGCGGCAATCTAGCTCTTAACCCCTCTCGAAGCCTCGGAACCTCGAACA	746
626	DB	TGTTGTTACGGCGGCAATCTAGCTCTTAACCCCTCTCGAAGCCTCGGAACCTCGAACA	685
747	QY	TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGAAACATGCACCGCACAACTTCGGCT	806
686	DB	TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGAAACATGCACCGCACAACTTCGGCT	745
807	QY	TCGGTTTCTCTATCTTCACATAAGCTCAAGCAGCAAGAGACCTTTTCAGCGGAAAGACCT	866
746	DB	TCGGTTTCTCTATCTTCACATAAGCTCAAGCAGCAAGAGACCTTTTCAGCGGAAAGACCT	805
867	QY	GTAAGCAGGAGCAAACTACAGAGAGCACCAGCTGCCCTCTCAAAATGTTCTCCAGGG	926
806	DB	GTAAGCAGGAGCAAACTACAGAGATGACCAAGCTGCCCTCTCAAAATGTTCTCCAGGG	865
927	QY	ATTATATATTGACCTCGTGGATGACACTATACACAAAGAAAGTGTGCTATATGGCT	986
866	DB	ATTATATATTGACCTCGTGGATGACACTATACACAAAGAAAGTGTGCTATATGGCT	925
987	QY	TAAAGCCAGTGCACCTCCCGTGGCGGGCCCATCAGAGCCGTGGCCATCAGAGTGCAC	1046
926	DB	TAAAGCCAGTGCACCTCCCGTGGCGGGCCCATCAGAGCCGTGGCCATCAGAGTGCAC	985
1047	QY	TGTAGTCATATCGGCATTCGCGACGCTCTTCTACTGTATGTGCGCAAGAACCAAG	1106
986	DB	TGTAGTCATATCGGCATTCGCGACGCTCTTCTACTGTATGTGCGCAAGAACCAAG	1045
1107	QY	AAAATATATATTCATATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACATCGCAGC	1166
1046	DB	AAAATATATATTCATATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACATCGCAGC	1105
1167	QY	TCCCAAGAGAGAGCTCCGCGCGCGCGGAGGTCTTCTCTGCTATTCAGTAAAGTG	1226
1106	DB	TCCCAAGAGAGAGCTCCGCGCGCGCGGAGGTCTTCTCTGCTATTCAGTAAAGTG	1165
1227	QY	GCCAGATCAGATGAATGTGCCAGTGTTCGCTACTCTCTCCAGGACTTCTGTGGCT	1286
1166	DB	GCCAGATCAGATGAATGTCTGCCAGTGTTCGCTACTCTCTCCAGGACTTCTGTGGCT	1285
1287	QY	GTGAGTGGCTCTGGACCTGTGGGAAGACTTCAGCTCTGTAGAGAGGCGCAGAGAGAT	1346
1226	DB	GTGAGTGGCTCTGGACCTGTGGGAAGACTTCAGCTCTGTAGAGAGGCGCAGAGAGAT	1285
1347	QY	GGTCAATCCAGAGATCCAGAGTCCCAAGTTCATATGCTGTTCTTCCAAAGGTATGA	1406
1286	DB	GGTCAATCCAGAGATCCAGAGTCCCAAGTTCATATGCTGTTCTTCCAAAGGTATGA	1345
1407	QY	AGTACTTTGTCGACAGAGAACTACAAACAAGAGAGGTGGCGGAGGCTCGGGGAAG	1466
1346	DB	AGTACTTTGTCGACAGAGAACTACAAACAAGAGAGGTGGCGGAGGCTCGGGGAAG	1405
1467	QY	GAGAGCTCTTCTGTTGGCGGTGTCAACCATTTGCCGAAAGCTCCGCCAGGCCAGCAGA	1526
1406	DB	GAGAGCTCTTCTGTTGGCGGTGTCAACCATTTGCCGAAAGCTCCGCCAGGCCAGCAGA	1465

1527	QY	GTTCGTCCGCGCGCTCAGCAAGTTTATTCGCGCTCTACTTTGATTTATCTCTCGAGGAG	1586
1466	DB	GTTCGTCCGCGCGCTCAGCAAGTTTATTCGCGCTCTACTTTGATTTATCTCTCGAGGAG	1525
1587	QY	ACGTCCCGCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGGACAACTCTTCCTCAGC	1646
1526	DB	ACGTCCCGCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGGACAACTCTTCCTCAGC	1585
1647	QY	TCGTGTTCCCACTTCGACTCTCCGAGACCAACGCGCTCCAGAGCGCGGGCAGCACACGGCAG	1706
1586	DB	TCGTGTTCCCACTTCGACTCTCCGAGACCAACGCGCTCCAGAGCGCGGGCAGCACACGGCAG	1645
1707	QY	AGGGCAGCAGAGAACTATCTCCGAGCAGAGTCAGGCGGTGCCCTATAGCTCGCCATTT	1766
1646	DB	AGGGCAGCAGAGAACTATCTCCGAGCAGAGTCAGGCGGTGCCCTATAGCTCGCCATTT	1705
1767	QY	GCAACATGCACCAAGTTATTGACGAGGAGCCGACCTGCTGTCGAAAGACGATTCGTTCCCT	1826
1706	DB	GCAACATGCACCAAGTTATTGACGAGGAGCCGACCTGCTGTCGAAAGACGATTCGTTCCCT	1765
1827	QY	TCCATCCTCTCCACTCGCTACCCGAGAGCCAGCTCTTGAGAAATTTGATTCGGGCTTGG	1886
1766	DB	TCCATCCTCTCCACTCGCTACCCGAGAGCCAGCTCTTGAGAAATTTGATTCGGGCTTGG	1825
1887	QY	TTTTAAATGATGTACTGTGCAACACGAGGCTCAGAGTGACTCTCGCTAAAGGTAGAGG	1946
1826	DB	TTTTAAATGATGTACTGTGCAACACGAGGCTCAGAGTGACTCTCGCTAAAGGTAGAGG	1885
1947	QY	CGGCTGTTCTGGGGCAACCGGACACGCGACTCCAGACAGAGAGTCAAGATGGGGGCC	2006
1886	DB	CGGCTGTTCTGGGGCAACCGGACACGCGACTCCAGACAGAGAGTCAAGATGGGGGCC	1945
2007	QY	TGGACCAAGCGGGGAGGCCGCGCTTCGCTTGACGCTGAGCGCGCTCGCAACCCCTGCG	2066
1946	DB	TGGACCAAGCGGGGAGGCCGCGCTTCGCTTGACGCTGAGCGCGCTCGCAACCCCTGCG	2005
2067	QY	TGCACACGGTGAAGACCGGCGAGCCCTCGACACATCGCGGGGACTCAGAGCATCTATGACT	2126
2006	DB	TGCACACGGTGAAGACCGGCGAGCCCTCGACACATCGCGGGGACTCAGAGCATCTATGACT	2065
2127	QY	CGTCTGTGCCCTCATCGAGCTGTCTCTGCGACTGATGGAGGACTCTCGAGCGACCA	2186
2066	DB	CGTCTGTGCCCTCATCGAGCTGTCTCTGCGACTGATGGAGGACTCTCGAGCGACCA	2125
2187	QY	CAGAAACGCTCTCCCTGACGGAGAGCGTGCTCTCTCTTCAGGCTCGGGTGAGGAGAAC	2246
2126	DB	CAGAAACGCTCTCCCTGACGGAGAGCGTGCTCTCTCTTCAGGCTCGGGTGAGGAGAAC	2185
2247	QY	CTCCTGCCCTCTCTTCCAAAGCTCTCTCTCTCGGGTCAATGCAAAAGACATCTTGTTGCC	2306
2186	DB	CTCCTGCCCTCTCTTCCAAAGCTCTCTCTCTCGGGTCAATGCAAAAGACATCTTGTTGCC	2245
2307	QY	GGAGCTACACTGATGAACTCCACGGGTGCGGCCCTTGTACAAACGAAAGACTCTAAG	2366
2246	DB	GGAGCTACACTGATGAACTCCACGGGTGCGGCCCTTGTACAAACGAAAGACTCTAAG	2305
2367	QY	CATTGCCACTTTAGCTG	2383
2306	DB		2322
		CATTGCCACTTTAGCTG	

RESULT 5	
AA151346	
ID	AA151346 standard; cDNA; 3083 BP.
XX	
XX	AA151346;
XX	
DT	13-FEB-2002' (first entry)
DT	
XX	
XX	DNA encoding human interleukin 17 (hIL-17) receptor like protein.
DE	
XX	Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW	

XX DNA encoding human Interleukin 17 (hIL-17) receptor like protein.  
DE  
XX  
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;







CC sclerosis, liver failure, hemorrhages, paranoia, obsessive compulsive  
 CC disorder, autism, panic disorder, learning disabilities, ALS  
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,  
 CC sleep patterns, balance, and perception. Phi-dependent insulin, adult  
 CC respiratory distress syndrome (ARDS). The secreted protein is further  
 CC useful for identifying compounds that bind to the secreted protein. The  
 CC present sequence encodes a novel secreted protein of the invention.  
 XX  
 SQ Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 other;

Query Match 90.6%; Score 2158.4; DB 24; Length 4392;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 2255; Conservative 0; Mismatches 1; Indels 46; Gaps 5;

QY	86	ATGCGCCCGCTGGCTGCAGCTCTGCTCGCTCTTCTTACGGTAAACCGCTCGCTCAACGGC	145
DB	1	ATGCGCCCGCTGGCTGCAGCTCTGCTCGCTCTTCTTACGGTAAACCGCTCGCTCAACGGC	60
QY	146	TGCGAGCTGCTGTGGCGCTGGGGGCTCGCGCGCGCGGGGCGCGACACCTGTGGC	205
DB	61	TGCGAGCTGCTGTGGCGCTGGGGGCTCGCGCGCGGGGCGCGACACCTGTGGC	120
QY	206	TGGAGGATGAAGCGGCTGCCCGACCCCGGCTTGTGCTTAATGAGGAGTGGGGCA	265
DB	121	TGGAG-----GGAGTGGGGCCA	138
QY	266	CCGACGAAACAGTGGGCTGTAAACATCACCTTTCAATATGACAAATGTACACCTAC	325
DB	139	CCGACGAAACAGTGGGCTGTAAACATCACCTTTCAATATGACAAATGTACACCTAC	198
QY	326	TTGAATCCAGTGGGGAAGCATGTGCTGAAGCGCCAGAAATATACCATCAGACCATAT	385
DB	199	TTGAATCCAGTGGGGAAGCATGTGCTGAAGCGCCAGAAATATACCATCAGACCATAT	258
QY	386	CTTGCCATGACCAAGTGGGAGTCAACATCTTTGGTCCCGAGGGCCCTCGGCATGAA	445
DB	259	CTTGCCATGACCAAGTGGGAGTCAACATCTTTGGTCCCGAGGGCCCTCGGCATGAA	318
QY	446	TTCTGAAAGGATTTCCGGTAACTTGGAGAGCTGAAGTGGGAGGAGAGAGTGGCAA	505
DB	319	TTCTGAAAGGATTTCCGGTAACTTGGAGAGCTGAAGTGGGAGGAGAGAGTGGCAA	378
QY	506	CAACTGATTTAAAGGATTCGGAAGCAGCTCAACAGTAGCTTCAAAAAGAACTGGAAATGAA	565
DB	379	CAACTGATTTAAAGGATTCGGAAGCAGCTCAACAGTAGCTTCAAAAAGAACTGGAAATGAA	438
QY	566	TCTCAACCTTTCTGAATATGAATTTGAACGGATATTTCGTAAGGTTGTCCTTTT	625
DB	439	TCTCAACCTTTCTGAATATGAATTTGAACGGATATTTCGTAAGGTTGTCCTTTT	498
QY	626	CTTTCATTAAAGCAAGCAATACACCTTTCTTCTTAGACCGAGCCTGTGAC	685
DB	499	CTTTCATTAAAGCAAGCAATACACCTTTCTTCTTAGACCGAGCCTGTGAC	558
QY	686	CTGTGTTACACCGGAGCAATCTAGCTTGAACCTTCTGGAAGCCTCGGAACCTGAAC	745
DB	559	CTGTGTTACACCGGAGCAATCTAGCTTGAACCTTCTGGAAGCCTCGGAACCTGAAC	618
QY	746	ATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGACCGCACAACTTCGGC	805
DB	619	ATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGACCGCACAACTTCGGC	678
QY	806	TTCCGTTTCTTCTATCTTCACTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAGACC	865
DB	679	TTCCGTTTCTTCTATCTTCACTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAGACC	738
QY	866	TGTAAAGCGAGCAACTACAGAGACGACCGCTGCTCTTCAAAATGTTTCTCCAGGG	925
DB	739	TGTAAAGCGAGCAACTACAGAGACGACCGCTGCTCTTCAAAATGTTTCTCCAGGG	798
QY	926	GATTATATAATTTAGCTGGTGGATGACACTAACACAAAGAAAGTATGATTTATGCC	985
DB	799	GATTATATAATTTAGCTGGTGGATGACACTAACACAAAGAAAGTATGATTTATGCC	858

QY	986	TTAAAGCCAGTGCATCCCGTGGGCGGCGCCCATCAGAGCGTGGCCATCAGATGCCA	1045
DB	859	TTAAAGCCAGTGCATCCCGTGGGCGGCGCCCATCAGAGCGTGGCCATCAGATGCCA	918
QY	1046	CTGGTAGTCATATCGGATTCGCGAGCTCTTCACTGTGATGTGGCGGAGAACACAA	1105
DB	919	CTGGTAGTCATATCGGATTCGCGAGCTCTTCACTGTGATGTGGCGGAGAACACAA	978
QY	1106	GAATATATATTCACATTTAGATGAAGAGAGCTCTGTAGTCTTCCACATACACTGCAGCA	1165
DB	979	GAATATATATTCACATTTAGATGAAGAGAGCTCTGTAGTCTTCCACATACACTGCAGCA	1038
QY	1166	CTCCAAAGAGAGAGCTCCGGCGCGGGCGGAGAGTCTTCTCTGTCTATTCCAGTAAAGAT	1225
DB	1039	CTCCAAAGAGAGAGCTCCGGCGCGGGCGGAGAGTCTTCTCTGTCTATTCCAGTAAAGAT	1098
QY	1226	GGCCAGATTCACATGAATGTCTCAGTGTCTTCCGCTACTTCTCCAGGACTCTGTGGC	1285
DB	1099	GGCCAGATTCACATGAATGTCTCAGTGTCTTCCGCTACTTCTCCAGGACTCTGTGGC	1158
QY	1286	TGTGAGTGGCTCTGGAGCTCTCGGGAAGACTTCAGCTCTGTAGAGAGAGGCGAGAGAA	1345
DB	1159	TGTGAGTGGCTCTGGAGCTCTCGGGAAGACTTCAGCTCTGTAGAGAGAGGCGAGAGAA	1218
QY	1346	TGGGTCTATCCAGAGATCCACGAGTCCCATTCATCATTTGTGTTTGTTCAAAAGTATG	1405
DB	1219	TGGGTCTATCCAGAGATCCACGAGTCCCATTCATCATTTGTGTTTGTTCAAAAGTATG	1278
QY	1406	AAGTACTTTTGTGGCAAGAAAGAACTACAAACACAAAGAGGTGGCGAGGCTCGGGGAAA	1465
DB	1279	AAGTACTTTTGTGGCAAGAAAGAACTACAAACACAAAGAGGTGGCGAGGCTCGGGGAAA	1338
QY	1466	GGAGAGCTCTTCTCGTGGCGGTGTCAGCCATTCGCCAAGAAAGCTCGCCAGCCAGCAG	1525
DB	1339	GGAGAGCTCTTCTCGTGGCGGTGTCAGCCATTCGCCAAGAAAGCTCGCCAGCCAGCAG	1398
QY	1526	AGTTCTCGCGCGGCTCAGCAAGTTTATCGCGCTCTACTTTGATTTATTTCTCGGAGGGA	1585
DB	1399	AGTTCTCGCGCGGCTCAGCAAGTTTATCGCGCTCTACTTTGATTTATTTCTCGGAGGGA	1458
QY	1586	GAGCTCCCGGCTATCTAGACCTAGTACCAAGTACAGACTCATGACAAATC-TTCCTCA	1644
DB	1459	GAGCTCCCGGCTATCTAGACCTAGTACCAAGTACAGACTCATGACAAATCTTTCCTCA	1518
QY	1645	GCTCTCTTCCCACT-TGCACTCCCGAGACCAAGCTCCAGAGCGCGGGCA-GCACACG	1702
DB	1519	GCTCTCTTCCCACTTGCACCTCCCGAGACCAAGCTCCAGAGCGCGGGCATGCACACG	1578
QY	1703	CGACAGGCA-GCAGAGAGAGTACTTCGGGAGCAAGTCAAGCGCTATACGTCCG	1761
DB	1579	CGACAGGCGGAGAGAGAGTACTTCGGGAGCAAGTCAAGCGCTATACGTCCG	1638
QY	1762	CATTTCACACATTCACACAGTTTATTCAGAGAGCCGACTGTTTCGAAAAGCAAGTTCGT	1821
DB	1639	CATTTCACACATTCACACAGTTTATTCAGAGAGAGCCGACTGTTTCGAAAAGCAAGTTCGT	1698
QY	1822	TCCCTTCCATCTCTCCATCGCTTACCGGAGCCAGCTCTTGGAGAAATTTGATTCGGG	1881
DB	1699	TCCCTTCCATCTCTCCATCGCTTACCGGAGAGCCGACTCTTGGAGAAATTTGATTCGGG	1758
QY	1882	CTTGTGTTTAAATGATGTATGTGCAACAGGCTTGAGAGTACTTCTCTCTAAAGGT	1941
DB	1759	CTTGTGTTTAAATGATGTATGTGCAACAGGCTTGAGAGTACTTCTCTCTAAAGGT	1818
QY	1942	AGAGCGGCTGTTTCTGGGCAACCGGAGCAGCTCCAGCAGAGAGTCAAGATG	2001
DB	1819	AGAGCGGCTGTTTCTGGGCAACCGGAGCAGCTCCAGCAGAGAGTCAAGATG	1878
QY	2002	GGGCTTGGACCAAGAGCGGAGCGCGGCTTGCCTTTGACGTAGCGCGGCGGCTTGAAC	2061
DB	1879	GGGCTTGGACCAAGAGCGGAGCGCGGCTTGCCTTTGACGTAGCGCGGCGGCTTGAAC	1938





Db 662 CCATGCTCGGACATGACGCTGTCTCGACCGCAGCAGCAACATTCGGCTTCGGTT 721  
 QY 813 TCTTCTATCTTCACTACAACTCAAGCAGGAGGACCTTTCAGCCCAAGACCTGTAGC 872  
 Db 722 TCTTCTATCTTCACTACAACTCAAGCAGGAGGACCTTTCAGCCCAAGACCTGTAGC 781  
 QY 873 AGGAGCAAACTACAGAGACGACGAGCTGCTCTTCAAAATGTTTCTCCAGGGATATA 932  
 Db 782 AGGAGCAAACTACAGAGATACGAGCTGCTCTTCAAAATGTTTCTCCAGGGATATA 841  
 QY 933 TAATTGAGCTGGTGGATGACATACACAAACAAAGAAAGTGATGCATTAATGCTTTAAGC 992  
 Db 842 TAATTGAGCTGGTGGATGACATTAACACAAACAAAGAAAGTGATGCATTAATGCTTTAAGC 901  
 QY 993 CAGTGCACTCCCGCTGGCGCGGCGCCATCAGAGCGCTGGCGCTTCACAGTGCCACTGGTAG 1052  
 Db 902 CAGTGCACTCCCGCTGGCGCGGCGCCATCAGAGCGCTGGCGCTTCACAGTGCCACTGGTAG 961  
 QY 1053 TCATATCGGCTTCCGAGAGCTCTTCACTGTGATGCTGCGCAAGAGCAACAGAAATA 1112  
 Db 962 TCATATCGGCTTCCGAGAGCTCTTCACTGTGATGCTGCGCAAGAGCAACAGAAATA 1021  
 QY 1113 TATATTCACATTTAGTGAAGAGAGCTCTGAGTCTTCCACATACATGACAGCTCCCAA 1172  
 Db 1082 TATATTCACATTTAGTGAAGAGAGCTCTGAGTCTTCCACATACATGACAGCTCCCAA 1081  
 QY 1173 GAGAGAGCTCCGCGCGCGCGGCGAGGCTCTTCTCTGCTATTCACGTAAGATGCGCAGA 1232  
 Db 1082 GAGAGAGCTCCGCGCGCGCGGCGAGGCTCTTCTCTGCTATTCACGTAAGATGCGCAGA 1141  
 QY 1233 ATCATATGAATTCGCTCCAGTGTTTGGCGCTACTTCTCCAGGACTTCTGTGGCTGTAGG 1292  
 Db 1142 ATCATATGAATTCGCTCCAGTGTTTGGCGCTACTTCTCCAGGACTTCTGTGGCTGTAGG 1201  
 QY 1293 TGGCTCTGGAGCTTGGCAAGCTTCCAGGCTCTGTAGAGAGGCGAGAGANTGGTCA 1352  
 Db 1202 TGGCTCTGGAGCTTGGCAAGCTTCCAGGCTCTGTAGAGAGGCGAGAGANTGGTCA 1261  
 QY 1353 TCCAGAGATTCACAGAGTCCGAGTCTCATCTTGTGGTGTGTTCNAAGTATGAAGTACT 1412  
 Db 1262 TCCAGAGATTCACAGAGTCCGAGTCTCATCTTGTGGTGTGTTCNAAGTATGAAGTACT 1321  
 QY 1413 TTGTGGACAAGAAAGTACAAACAAAGAGAGTGGCGGAGGCTCGGGGAAAGGAGAGC 1472  
 Db 1322 TTGTGGACAAGAAAGTACAAACAAAGAGAGTGGCGGAGGCTCGGGGAAAGGAGAGC 1381  
 QY 1473 TCTTCTGTGGCGGTGTACGCCATTTGCCAAAAGCTCGCGCAGGCGCAAGCAGAGTTCGT 1532  
 Db 1382 TCTTCTGTGGCGGTGTACGCCATTTGCCAAAAGCTCGCGCAGGCGCAAGCAGAGTTCGT 1441  
 QY 1533 CCGCGGCGCTCAGCAAGTTATTCGCGTCTACTTTGATTATTCCTCGAGGAGACGCTCC 1592  
 Db 1442 CCGCGGCGCTCAGCAAGTTATTCGCGTCTACTTTGATTATTCCTCGAGGAGACGCTCC 1501  
 QY 1593 CCGGTATCTAGACCTGATACAGTACAGCTATGAGCAATCTTCTCAGCTCTGTT 1652  
 Db 1502 CCGGTATCTAGACCTGATACAGTACAGCTATGAGCAATCTTCTCAGCTCTGTT 1561  
 QY 1653 CCCACTTGCACCTCCGAGACCGGCTCCAGGAGCGGGGCGAGCAGACGCGCAGAGGCA 1712  
 Db 1562 CCCACTTGCACCTCCGAGACCGGCTCCAGGAGCGGGGCGAGCAGACGCGCAGAGGCA 1621  
 QY 1713 GCAGAGGAAGTACTTCCGAGCAAGTTCAGGCGGCTCCCTATACGTCGCGCATTTGCAACA 1772  
 Db 1622 GCAGAGGAAGTACTTCCGAGCAAGTTCAGGCGGCTCCCTATACGTCGCGCATTTGCAACA 1681  
 QY 1773 TGCACAGTTTATTCAGGAGCGCGCTGTTTCGAAAGAGGCTGCTTCCCTCCATC 1832  
 Db 1682 TGCACAGTTTATTCAGGAGCGCGCTGTTTCGAAAGAGGCTGCTTCCCTCCATC 1741  
 QY 1833 CTCCTCCACTGCGCTACCGGAGCGCAGTCTTCGAGAAATTTGATCGGCTTGGTTTAA 1892  
 Db 1742 CTCCTCCACTGCGCTACCGGAGCGCAGTCTTCGAGAAATTTGATCGGCTTGGTTTAA 1801

QY 1893 ATCATCTATGTGCAAAACAGGCGCTGAGAGTGAATCTTCCCTAAAGGTAGAGCGGCTG 1952  
 Db 1802 ATCATCTATGTGCAAAACAGGCGCTGAGAGTGAATCTTCCCTAAAGGTAGAGCGGCTG 1861  
 QY 1953 TTCTTGGGCGCAACCGGAGCAGCAGCTCCAGCAGCAGAGAGTCAAGATGAGGCGCTTGACC 2012  
 Db 1862 TTCTTGGGCGCAACCGGAGCAGCAGCTCCAGCAGCAGAGAGTCAAGATGAGGCGCTTGACC 1921  
 QY 2013 AAGACGGGAGGCGCGGCGCTTGGAGCTGAGGCTGAGGCGCGCTTGCMAACCCCTTGTGACA 2072  
 Db 1922 AAGACGGGAGGCGCGGCGCTTGGAGCTGAGGCTGAGGCGCGCTTGCMAACCCCTTGTGACA 1981  
 QY 2073 CGGTAAAGCGGCGAGCGCTTGGAGCTGAGGCTGAGGCGCGCTTGCMAACCCCTTGTGACA 2132  
 Db 1982 CGGTAAAGCGGCGAGCGCTTGGAGCTGAGGCTGAGGCGCGCTTGCMAACCCCTTGTGACA 2041  
 QY 2133 TGGCTCTATCCGAGCTGCTTCCGACTGATGAGGAGTCTCGAGCGGAGCAGACAGA 2192  
 Db 2042 TGGCTCTATCCGAGCTGCTTCCGACTGATGAGGAGTCTCGAGCGGAGCAGACAGA 2101  
 QY 2193 CGTCTTCCCTGACGAGAGGCTGCTTCCGACTGATGAGGAGTCTCGAGCGGAGCAGCCTCG 2252  
 Db 2102 CGTCTTCCCTGACGAGAGGCTGCTTCCGACTGATGAGGAGTCTCGAGCGGAGCAGCCTCG 2161  
 QY 2253 CCCTTCTTCCAAAGCTCTCTTCTGGGTGATGCAAGCAGAGTCTTGTGGCGGAGCT 2312  
 Db 2162 CCCTTCTTCCAAAGCTCTCTTCTGGGTGATGCAAGCAGAGTCTTGTGGCGGAGCT 2221  
 QY 2313 ACACATGATGAATCTCAGCGGCTGCGCTTGTGAGCAAAAGAGTCTTAAGCATTGC 2372  
 Db 2222 ACACATGATGAATCTCAGCGGCTGCGCTTGTGAGCAAAAGAGTCTTAAGCATTGC 2281  
 QY 2373 CACTTTA.2379  
 Db 2282 CACTTTA.2288

## RESULT 8

ABA95037

ID ABA95037 standard; DNA; 2443 BP.

XX ABA95037;

XX AC ABA95037;

XX DT 20-MAY-2002 (first entry)

XX Murine cytokine receptor, zcytor18 nucleotide sequence.

XX Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;

XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;

XX erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.

XX OS Mus sp.

XX Key Location/Qualifiers

XX CDS 101..2320

XX FT /\*tag= a

XX FT /product= "mouse zcytor18"

XX PN W0200208259-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-US23253.

XX PR 26-JUL-2000; 2000US-220747P.

XX PA (ZYMO.) ZYMOGENETICS INC.

XX PI Presnell SR, Kuestner RE, Gao Z;

XX DR WPI; 2002-217048/27.

XX P-PSDB; ABB07630.

XX New cytokine receptor polypeptide designated zcytor18, useful for  
 PT inhibiting cell proliferation associated with psoriasis or tumor  
 PT growth, and modulating immune system by binding to endogenous zcytor18  
 PT ligand

PS Claim 7; Page 111-115; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumor growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC murine zcytor18 nucleotide sequence.

XX Sequence 2443 BP; 564 A; 700 C; 642 G; 537 T; 0 other;

Query Match 68.8%; Score 1638.4; DB 24; Length 2443;  
 Best Local Similarity 82.5%; Pred. No. 0;  
 Matches 1976; Conservative 0; Mismatches 356; Indels 64; Gaps 6;

QY 1 CCGCGCGGCGCACCGCCACCTCGGGGCT---GGCCAGCGCGCGCGCGCGCGGCGGCGAGA 56  
 DB 12 CCGCTACACCGCGCGCGCCACTCGGGAGTAGAGAGCGAGCTACAGGCGAGCAACCTAGCGGA 71  
 QY 57 GAACGGCTGGCTGGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 116  
 DB 72 GACCG 131  
 QY 117 TCCTTAGGTCAACCGCTGCGCTCAACGGCTGCGAGCTGGCTGGCGCGCGCGCGCGCGCGCG 176  
 DB 132 TCCTTAGGTCAACCGCTGCTCAACGGCTGCGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCG 191  
 QY 177 GCG 236  
 DB 192 GCG 225  
 QY 237 TTTGTGTCTTAATGAGGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 296  
 DB 226 -----GGAGTGGGCG 269  
 QY 297 CCTTAAATGACAAATGTACCACTACTTCAATCCAGT---GGGGAAGCATGTGATTG 353  
 DB 270 CCTTCAATGACAAATGTACCACTACTTCAATCCAGT---GGGGAAGCATGTGATTG 329  
 QY 354 CTGACG 413  
 DB 330 CTGATGCTCAGAACATCACCATCAGCCAGTACGCTTGGCCAGCAGCGAGGTGGCGAGTCA 389  
 QY 414 TTTCTTGTGTCGCCAGGCG 473  
 DB 390 TTTCTTGTGTCGCCAGGCG 449  
 QY 474 AGGAGCTGAAGTTCGGGCGGAGAGCTGCCAGCACTGATTTCAAGGATCCGAGGAGC 533  
 DB 450 AGGAGCTGAAGTTCGGGCGGAGAGCTGCCAGCACTGATTTCAAGGATCCGAGGAGC 509  
 QY 534 TCAACAGTACGCTTCAAGAGACTGGGAATCTCAACCTTTCTTGAATATGAATTTG 593  
 DB 510 TCAACAGTACGCTTCAAGAGACTGGGAATCTCAACCTTTCTTGAATATGAATTTG 569  
 QY 594 AAACGGATTTATTCCTAAAGGTTGTCCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 653  
 DB 570 AGACGGATTTATTCCTAAAGGTTGTCCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 629

QY 554 ACCCTTCTTCTTTAGAACCGGAGCGCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 713  
 DB 630 ATCCCTTCTTCTTTCAGAACGAGGCGCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 689  
 QY 714 GTAAACCTTCTTGTGAAGCTCGGAACCTGAACATCAGCCAGCATGCTCGGACATCGAGG 773  
 DB 690 GTAAAGCTTCTTGTGAAGCTCGGAACCTGAATATATCAGCCAGCATGGTCTGACATCGACG 749  
 QY 774 TGTCTTTCAGCATGCAACCGCAACTTCGGCTTCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 833  
 DB 750 TGTCTTTCAGCATGCAACCGCAACTTCGGCTTCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 809  
 QY 834 TCAGCAGCAGCACTTTCAGGGAAGAGCTGTAGGAGAGCTGTAGGAGAGCAACTACAGAGCA 893  
 DB 810 TCAGCAGCAGCACTTTCAGGGAAGAGCTGTAGGAGAGCTGTAGGAGAGCAACTACAGAGCA 869  
 QY 894 CCAAGTCCCTTCTTCAAAATGTTTCTCCAGGGATATATATTAATGAGCTGTGGATGACA 953  
 DB 870 CCAAGTCCCTTCTTCAAAATGTTTCTCCAGGGATATATATTAATGAGCTGTGGATGACA 929  
 QY 954 CTAAACACAAAGAAAGTATGATATATGCTTAAAGCCAGTGCACCTCCCGCTGGGCGG 1013  
 DB 930 GCAACACCAAGAAAGTATGATATATGCTTAAAGCCAGTGCACCTCCCGCTGGGCGG 989  
 QY 1014 GCGCCATCAGAGCGGTGGCCATCAGAGTGCACCTGCTAGTATATCGGATTCGCGAGCG 1073  
 DB 990 GACCCATCAGAGCGGTGGCCATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1049  
 QY 1074 TCTTCACTGTGATGTCGCGCAAGCAAGCAACAGCAAGCAATATATATCAATGATGATGAG 1133  
 DB 1050 TGTTCATCTGTGATGTCGCGCAAGCAAGCAACAGCAAGCAATATATATCAATGATGATGAG 1109  
 QY 1134 AGAGCTGTGATGTCGCGCAAGCAAGCAACAGCAAGCAATATATATCAATGATGATGAG 1193  
 DB 1110 AAAGCGGAGTGTGTCACATACGCTGCGGCTCTCCCGCAGAGAGCTGCGGCGCTCAGC 1169  
 QY 1194 CGAAGTCTTCTTCTGCTTATTCAGTAAAGATGCGCAAGATCAATGATGCTGCTCAGT 1253  
 DB 1170 CCAAGTCTTCTTCTGCTTATTCAGTAAAGATGCGCAAGATCAATGATGCTGCTCAGT 1229  
 QY 1254 GTTTCGCTTCTTCTTCTGCTTATTCAGTAAAGATGCGCAAGATCAATGATGCTGCTCAGT 1313  
 DB 1230 GTTTCGCTTCTTCTTCTGCTTATTCAGTAAAGATGCGCAAGATCAATGATGCTGCTCAGT 1289  
 QY 1314 ACTTCAAGCTCTGTAGAGAGGCGAGAGATGGTTCATCCAGAGATTCACAGGATTCACG 1373  
 DB 1290 ATTTCAAGCTCTGTAGAGAGGCGAGAGATGGTTCATCCAGAGATTCACAGGATTCACG 1349  
 QY 1374 AGTTCAATCTGCTGCTTGTTCAGAGGATGAGAGTACTTTGTGGAGAGAGAGTACTA 1433  
 DB 1350 AGTTCAATCTGCTGCTTGTTCAGAGGATGAGAGTACTTTGTGGAGAGAGAGTACTA 1409  
 QY 1434 AACACAAAGAGGTGGCGGAGGCTCGGGGAAAGAGAGCTCTTCTGCTGGCGGCTGTCAG 1493  
 DB 1410 GACACAAAGAGGCGCGCGCGGAGGCGCAAGGAGTCTTCTGCTGGCGGCTGTCAG 1469  
 QY 1494 CCAATGCGGAAAGCTCCGCGAGGCAAGAGAGTCTGCTCGCGGCTGTCAGAGTTTA 1553  
 DB 1470 CCAATGCGGAGAGCTCCGCGAGGCAAGAGAGTCTGCTCGCGGCTGTCAGAGTTTA 1529  
 QY 1554 TCAGCGCTTACTTGTATTTATTCCTGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1613  
 DB 1530 TCAGCGCTTACTTGTATTTATTCCTGGAGGAGAGTACCTGCGAGCTGCTGCTGCTGCTG 1589  
 QY 1614 CCAAGTACAGACTCATGACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1673  
 DB 1590 CCAAGTACAGACTCATGACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1649  
 QY 1674 ACAGCGCTCCAGCGCGGCGGAGAGCTGCGCGAGGCGAGGCGAGGAGAGTACTTCTCGGA 1733  
 DB 1650 AGG-----AGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1703  
 QY 1734 GCAAGTACAGCGCGGCTCCCTATAGCTGCGGCTTTCGACATGCGACAGCTTTTATGACAGG 1793





Disclosure; Page 101-102; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 *in vivo* gene therapy techniques. Zcytor18 oligonucleotide probes are useful for *in vivo* diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissues/samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinolipidosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 variant degenerate coding sequence.

Sequence 2259 BP.; 379 A; 234 C; 374 G; 293 T; 979 other;

	Query Match	67.6%	Score	1612;	DB	24;	Length	2259;	
	Best Local Similarity	56.6%;	Pred.	No. 0;					
	Matches 1278;	Conservative	576;	Mismatches	404;	Indels	0;	Gaps	0;
QY	86	ATGGCCCCGTGCGTGCAGCTCTGCTCGTCCTTTACGGTCAACGCCCTGCCTCAACGGC	145						
DB	1	ATGGCCNCGTGTCNCARVNTGVWSNGTNTVTYYACNGTNAAYGONTGYTNAYGNN	60						
QY	146	TCCAGCTGGCTGTGGCCGCTGCGGGGTGCGCGCGCGCGGGCGCGCACACCTGTGTGC	205						
DB	61	WNCARYTNGCNTNGCNCGNGGNWNSNGMNGNCGNMNGNCGNENAYACTGTGYN	120						
QY	206	TGAGGATGAAGAGCGCTGCCCGACC CGCGCTTGTGTGCTAATGAGCGACTGGGGCCA	265						
DB	121	TGGMGNTGAARGCNGCNGWCNCGNHYTWYGTNGCNAAYGARNGNTGGNCCN	180						
QY	266	GCCAGCAGAACAAGCTGGCGCTGTACACACCATCTCAANTATGACAAATTGACACCTAC	325						
DB	181	GCWSHMGNAATWBSGNTNTATATATHACNTTYTAATAYGATYAATGYACANMCATY	240						
QY	326	TTGAATCCAGTGGGGAGCANOTGATTCCTTGACGCCAGATAATCACCATCAGCCAGAT	385						
DB	241	YTNAYTCCNGTNGMAARCAIYGATNHCGNGAYGCNCARAAYATHACNATHWSNCARTAY	300						
QY	386	GCTTGCCATGACCAGTGGCAGTCACCAATCTTTGGTCCCAGGGGCCCTCGGCATCGAA	445						
DB	301	GCMTGTCAYGAYCARGTNGCNGTNCANATHYTWGWSCNCCNGGNGCNTINGNATHGAR	360						
QY	446	TTCTGAAGAGATTCGGGTAACTCTGGAGGAGCTGAAGTCGGAGGAGAGACAGTGCCAA	505						
DB	361	TTTTNAARGGNTYINGNTNATHYTINGARGRYTNAARWSNGARGSNNGNCARTGYCAR	420						
QY	506	CAACTGATCTAAAGGATCGGAAGCAGCTCAACAGTAGCTTCAAAAGACATGGATGAA	565						
DB	421	CARYTNATHYNAARGAYCCNARCARYTNAAYWSNWTYYAARMGNACNGNATGGAR	480						
QY	566	TCFCAACCTTCTCGAATATGAATTTGAAACGGATATATTCGTGAAGGTTGTCCTCTTT	625						
DB	481	WSCARCCNTTYTNAAYATGAARTYTGARACNGATYATYTYGTNAARNTGNCNCTTY	540						
QY	626	CCTTCATTAAAAACGAAAGCAATTAACACCTCTTCTCTTTAGAACCCGACGCTGTGAC	685						
DB	541	CCNWSNATHAARAAYGARWSNAAYTATCATCTCNTTYTTYTYTMGNACNMGNCNTGTGAY	600						
QY	686	CTGTGTTACAGCGGACAACTACGTTGTGAACCCCTTCGGAAGCCTCGGAACCTGAAC	745						
DB	601	YTNWYTNARCACNGAYAAYTYNCGNTGYAARCCNTTYTGAARCCNMGNAAYTNAAY	660						
QY	746	ATCAGCGCAGCATGCTCGGCNATCGNGTGTCTTCGACCACTACCGCAGCAACTCGGC	805						
DB	661	ATHSNCARCAYGWNSNGNATGCAAGTWSNWTYYGATCACTCCNCAQYANYTTTGGN	720						
QY	806	TTGGTTCTTCTATCTTCACTACAGCTCAAGCAGGAGGACCTTTCAAGCGAAGAC	865						





[illegible]

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding/antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents human DCRS8 reverse translation generic cDNA.

Sequence 2214 BP; 371 A; 223 C; 358 G; 287 T; 975 other;







QY 1223 GATGGCCAGCAATGATGCTGCTCAAGTGTTCGCTACTTCTCCAGGACTTCTGT 1282  
 DB 1099 GATGGCCAGCAATGATGCTGCTCAAGTGTTCGCTACTTCTCCAGGACTTCTGT 1158  
 QY 1283 GCTGTGAGTGGCTCTGCGACCTGTGGAGACTTCAGCCCTCTGTAGAGAGGGCAGAGA 1342  
 DB 1159 GGTGTGAGTGGCTCTGCGACCTGTGGAGACTTCAGCCCTCTGTAGAGAGGGCAGAGA 1218  
 QY 1343 GAATGGGTCAATCCAGAGATCCAGAGTCCAGTTCATCATCTGTGTTTGTTCCTCAAGGT 1402  
 DB 1219 GATGGCCAGCAATGATGCTGCTCAAGTGTTCGCTACTTCTCCAGGACTTCTGT 1278  
 QY 1403 ATGAAGTACTTGTGGAGAGAACTACAAACAGAGAGGTGGCGAGCTCGGG 1462  
 DB 1279 ATGAAGTACTTGTGGAGAGAACTACAAACAGAGAGGTGGCGAGCTCGGG 1338  
 QY 1463 AAAGGAGCTCTTCTGCGGTGTCAGCCATTCGCAAGCTCCGACAGCCAG 1522  
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 QY 1523 CAGAGTCTCGCGGCTCAGCAAGTTTATCCCTCTACTTCTGATTTCTCGGAG 1582  
 DB 1399 CAGGNGARTTCTTCTGCGGTGTCAGCCATTCGCAAGCTCCGACAGCCAG 1458  
 QY 1583 GGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAATCTTCT 1642  
 DB 1459 GGNAGTATCCCTGAGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAATCTTCT 1518  
 QY 1643 CAGCTCTGTTCCACTTGTCCAGTCCGAGACCAAGTCCAGGAGCGGCGACACAG 1702  
 DB 1519 GARYTGTGTCNATTCATTCAGTCCGAGTCCGAGACCAAGTCCAGGAGCGGCGACACAG 1572  
 QY 1703 CGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAATCTTCT 1762  
 DB 1573 GGNATYNSWNGNGNATTCATTCAGTCCGAGTCCGAGACCAAGTCCAGGAGCGGCGACACAG 1632  
 QY 1763 ATTGCAATGACCAAGTATTCAGGAGGAGCGGCGAGTCTGGAAGACAGTCTGTT 1822  
 DB 1633 ATGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692  
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 DB 1813 GAGGCGCTGTTCTGCGGCGACCGGCGACCGGCGACCGGCGACCGGCGACCGGCGACCGG 1872  
 QY 1997 GATGGGCGCTGAGCAAGAGCGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2056  
 DB 1873 CATGTGNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGT 1932  
 QY 2057 CAACCGCTGCTGCAAGCTGAAAGCGGCGAGCGGCGAGTCCGAGTCCGAGTCCGAGTCCGAG 2116  
 DB 1933 CAACCGCTGCTGCAAGCTGAAAGCGGCGAGCGGCGAGTCCGAGTCCGAGTCCGAGTCCGAG 1992  
 QY 2117 ATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2176  
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 DB 2113 GAG 2169

QY 2297 CTGTGTTCCGACGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343  
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 RESULT 14  
 AAS16201  
 ID - AAS16201 standard; cDNA; 960 BP.  
 AC AAS16201;  
 XX 13-FEB-2002 (first entry)  
 XX 5' portion of Human interleukin 17 (hIL-17) receptor-like cDNA.  
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 75..960  
 XX /\*tag= a  
 XX /product= "hIL-17 receptor-like protein N-terminal"  
 XX /note= "Human Interleukin 17"  
 XX /partial.  
 XX /note= "No start or stop codon given"  
 XX /transl\_except= (pos:960, aa:Pro)  
 XX /note= "This codon is incomplete, as nucleotides  
 XX 961-3720 of Figure 1 are missing in the  
 XX specification."  
 XX WC200168859-A2.  
 XX PD 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX Jing S;  
 XX WPI; 2001-611392/70.  
 XX P-PSDB; AAU10601.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
 XX diabetes, psoriasis and glaucoma.  
 XX Claim 1; Fig 1; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease



Db 1384 GTCAGAGCAGGAGATGTTGAGAGCAACTCTAAGATCATCTCTCTGTCTCCGCGGCA 1443  
Qy 1404 TGAAGTACTTTGTGACAGAGAGACTACAAACACANAGAGGTGCGGAGGCTCGGGA 1463  
Db 1444 CGGCGCCCAAGTGGCAGGCGCTCTGGGCGGGGGGGCGCTGTGGCGCTGGCTGGCACC 1503  
Qy 1464 AAGGAGGCTCTCTCTGGTGGGCGGTGTGAGCCATTTGCCAAAGCTCGGCGAGGCCAAGC 1523  
Db 1504 ACGGAAAGCCGTTGGGGAGCTGTTCATCTGAGCCATGAACATGATCTCCGCACTTCA 1563  
Qy 1524 AGAGTTCTCGCGGCGCTCAGCAAGTTTATCGCCGCTCTACTTTGATTATTCTCTGGAGG 1583  
Db 1564 AGAGGCCAGCCTGCTTGGCACCTAGTAGTCTCTACTTACGCGAGGTCAAGTGTGACG 1623  
Qy 1584 GAGACTCTCCGCTATCTAGACTGAGTACCAAGTACAGCTCATGGACAACTTCTCTC 1643  
Db 1624 GCGAGTCTCCGACCTGTTCGGGCGGCGCGCGGTACCGCTCATGACAGGTTGAGG 1683  
Qy 1644 AGCTCTGTTCCTGCTGCTCGGAGCAGCGCTCCAGGAGCGGGGCGAGCACAGC 1703  
Db 1684 AGGTGACTTCCGATCCAGGACTGGAGATGTTCCAGCGGGCGCGATGCAACGGGTAG 1743  
Qy 1704 GACAGGCGAGAGAGAACTACTTCCGGAGCAAGTCAGCGCGGTCCCTATAGTCCCA 1763  
Db 1744 GGGAGCTGTCCGGGGAGAACTACTTCCGGAGCGCGGCGGCGAGGAGCTCGCGCGGCC 1803  
Qy 1764 TTTGCAACATGCACAGTTTATTTAGCAGGAGCGGAGTGGTTCCGAAAGCAGTTGTTTC 1823  
Db 1804 TGGACAGGTTCCGGGACTGSCAGGTCCGCTGTCCGACTGGTTGGAATGTGAGAACTCT 1863  
Qy 1824 CCT 1826  
Db 1864 ACT 1866

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GenCore version 5.1.4.p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: May 12, 2003, 10:35:26 ; Search time 2245 Seconds  
(without alignments)  
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Title: US-09-912-157-1

Perfect score: 2383

Sequence: 1 ccgcgcgcgcacccac.....aagcatgcccactttagctg 2383

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33208132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em\_estha.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
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7: em\_estro.\*  
8: em\_esti.\*  
9: gb\_est2.\*  
10: gb\_est3.\*  
11: gb\_est4.\*  
12: gb\_est5.\*  
13: gb\_est6.\*  
14: gb\_est7.\*  
15: em\_estom.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_othr.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	433	18.2	665 10	BB641245
3	431	18.1	547 12	BE750478
4	375.8	15.8	390 9	AA778029
5	351.8	14.8	377 12	BF803798
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RESULT 1  
BB616055  
LOCUS  
DEFINITION  
BB616055  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BB616055 649 bp mRNA linear EST-26-OCT-2001-  
BB616055 RIKEN full-length enriched, adult male testis Mus musculus  
cDNA clone 4931403M23.5', mRNA sequence.

BB616055  
GI:16456248

house mouse

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 649)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harada, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawa, J., Konno, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okada, K., Okazaki, F., Okido, T., Saito, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

TITLE  
JOURNAL  
COMMENT

## ALIGNMENTS

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JOURNAL  
MEDLINE  
COMMENT

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/getentry.pl?lib=MR06st2-MR0-CI0075-  
021100-003-c02st3-2000-11-02st4-1)  
Seq primer: puc 18 forward 377.  
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FEATURES  
source

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Site 2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 106 a 98 c 87 g 86 t

Query Match 14.8; Score 351.8; DB 12; Length 377.  
Best Local Similarity 99.4; Pred. No. 2.5e-81;  
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QY 951 ACTATACACACAGAGAGAGTATGCTTAAAGCCAGTGCACCTCCCGTGG 1010  
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RESULT 6  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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AM645591  
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EST  
African clawed frog.  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus  
1 (bases 1 to 627)  
Blackshear, P.J., Lai, W.S., Thord, J.M., Kennington, E.A., Staffa, N.G.  
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman  
J.W., Bonaldo, M.F., and Soares, M.B.  
The NIEHS Xenopus maternal EST project: interim analysis of the  
first 13,879 ESTs from unfertilized eggs  
Gene 267 (1), 71-87 (2001)  
21211403  
Contact: Perry J. Blackshear  
Office of Clinical Research and Laboratory of Signal Transduction  
National Institute of Environmental Health Sciences  
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,  
USA  
Tel: 919 541-4899  
Fax: 919 541-4571  
Email: black009niehs.nih.gov  
Clone is available through Research Genetics, Inc., 2130 Memorial  
Parkway, Huntsville, AL 35901  
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email  
cdna@resgen.com  
DNA Sequencing and analyses performed by National Institutes of  
Health-Intramural Sequencing Center (NISC).  
PCR Primers  
FORWARD: TGTAACACAGCGCCAGT  
BACKWARD: CAGGAACAGCTATGACC  
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/note="Vector: pT73-Pac; Site: 1: EcoRI; Site 2: NotI;  
PolyA-selected mRNA was prepared from unfertilized Xenopus  
laevis eggs. The library was constructed in the vector  
pT73-Pac as described in Bonaldo, M.F., Lennon, G., and  
Soares, M.B. Normalization and subtraction: two  
approaches to facilitate gene discovery, Genome Research  
6:791-806, 1996. The first strand synthesis used a  
NotI-drl8 primer; double-stranded cDNAs were ligated to  
EcoRI adapters, digested with NotI, and directionally  
cloned into the NotI and EcoRI-digested pT73-Pac vector.  
The library contained approximately 7.2 x 10<sup>5</sup>  
recombinants, with average insert sizes of 1-1.5 kb."

FEATURES  
source

BASE COUNT 172 a 159 c 153 g 143 t  
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Matches 436; Conservative 0; Mismatches 184; Indels 0; Gaps 0;  
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QY 389 TGCATGACCAAGTGGGAGTGCACATTTCTTTGGTCCCGAGGGCCCTCGGCATCGAATTC 448  
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QY 449 CTGAAGAGATTTGGGCTATACCTGGAGGAGCTGAAGTGGGAGGAGAGACATGCCACAA 508

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QY 629 TCCATTAAACGAAGCAATTTACACCTTTCTTTTGAAGCCGAGCCTGTGACCTG 688
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QY 689 TTGTTACAGCGGAGCAATCTAGCTTGTAAACCTTCTGGAAGCTCGGACCTGAACATC 748
Db 423 TTGTTACAGCGGAGCAATCTAGCTTGTAAACCTTCTGGAAGCTCGGACCTGAACATC 482
QY 749 AGCAGAGTCTGCGGACATGCTGCTGCGACATGCGAGCAGCTGCGGACATGCGGTC 808
Db 483 ACCCAACAGCGGCTGACATGAGTGTCTTTCAGCGGCGCCCTCGGAATTTGCGTTT 542
QY 809 COTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 868
Db 543 AACTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 602
QY 869 AAGCAGGCAAACTACAGA 888
Db 603 CGCAGGCTCTGAACACGGA 622

```

```

RESULT 7
Bg721995 602698761F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4830807 5',
LOCUS mRNA sequence.
DEFINITION Bg721995 577 bp mRNA linear EST 09-MAY-2001
ACCESSION Bg721995
VERSION Bg721995.1 GI:14001182
KEYWORDS EST:
SOURCE Human.
ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10752 row 1 column 16
High quality sequence stop: 576.
Location/Qualifiers
1. .577
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830807"
/clone.lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site: BamHI; Site 2: SalI-XhoI (gtcag
); Oligo-primed using primer 5'-TTTTTTTTTTTTTTT-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the

```

```

FEATURES
source

```

```

BASE COUNT 155 a 136 c 166 g 120 t
ORIGIN

```

```

Query Match 13.6% Score 325.2; DB 12; Length 577;
Best Local Similarity 92.4%; Pred. No. 3.2e-74;
Matches 353; Conservative 0; Mismatches 28; Indels 1; Gaps 1;
QY 208 GAGGATGAAGAGGGGCTGCCGACCCCGGGCTTTGTGTCTTAATGAGGAGTGGGCCAGC 267
Db 196 GTGGCTGAAGAGTGTGACTGGACTAGAGCAATCTTGGCTTGCAGGGAGTGGGCCAGC 255
QY 268 CAGCAGAAACAGTGGCTGTACACATCACTTTCAATATGACAAATGTACCACTACTT 327
Db 256 CAGCAGAAACAGTGGCTGTACACATCACTTTCAATATGACAAATGTACCACTACTT 315
QY 328 GAATCCAGTGGGGAAGCATGTGATGCTGACGCCAGAAATATCATCAGCCAGTATGC 387
Db 316 GAATCCAGTGGGGAAGCATGTGATGCTGACGCCAGAAATATCATCAGCCAGTATGC 375
QY 388 TTGCATGACCAAGTGGCAGTCACCAATCTTTGGTCCCGAGGGCCCTCGGCATCGAAT 447
Db 376 TTGCATGACCAAGTGGCAGTCACCAATCTTTGGTCCCGAGGGCCCTCGGCATCGAAT 435
QY 448 CCTGAAA-GGATTTCCGGTAACTACTGAGGAGCTGAAGTCGGAGGGAAGACAGTGCACAAC 506
Db 436 CCTGAAAAGGATTTCCGGTAACTACTGAGGAGCTGAAGTCGGAGGGAAGACAGTGCACAAC 495
QY 507 AACTGATTTCTTAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGCTGAATGAAT 566
Db 496 AACTGATTTCTTAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGCTGAATGAAT 555
QY 567 CTCAACCTTTCTTGAATGAATGA 588
Db 556 CTCAACCTTTCTTGAATGAATGA 577

```

```

RESULT 8
Bg263921 680 bp mRNA linear EST 24-OCT-2001
LOCUS Bg263921 RIKEN full-length enriched, 10 days neonate cortex Mus
DEFINITION musculus CDNA clone AB3001313 3', mRNA sequence.
ACCESSION Bg263921
VERSION Bg263921.2 GI:16400169
KEYWORDS EST:
SOURCE house mouse.
ORGANISM Mus musculus

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
M., Koya, S., Mori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jul 7, 2000 this sequence version replaced gi:8960377.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

```

```

Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library.
155 a 136 c 166 g 120 t

```

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10): 1617-1630 (2000)  
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. *Genome Res.* 10 (11): 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2): 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K. I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)  
 Please visit our web site (<http://genome-gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

## FEATURES

## Location/Qualifiers

1: 580  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_lib="RIKEN full-length enriched, 10 days neonate cortex"  
 /tissue\_type="cortex"  
 /dev\_stage="10 days neonate"  
 /lab\_host="DH10B"  
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 20.0 and subtraction to Rot - 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTAAATTAATCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified plasmidscript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 203 a 171 c 146 g 159 t 1 others  
 ORIGIN  
 Query Match 13.4%; Score 318.2; DB 10; Length 680;  
 Best Local Similarity 88.8%; Pred. No. 2.4e-72;  
 Matches 355; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Qy 278 AGTGGCGTACACATCCTCAATATGACAAATGTACACCTACTTGAATCCAGTG 337  
 Db 1 AGCGGACTGCACATCA-CCTGATAGACACCACTGTACACCTACTTGAATCCGCGG 59  
 Qy 338 GGGAGCATGTGATGTGAGCGCCAGATATCACCATCAGCAGTATGCTTGCATGAC 397  
 Db 60 GGGAGCATGTGATGTGATGCTCAGAACATCACCATCAGCAGTATGCTTGCATGAC 119  
 Qy 398 CAATGGCAGTCACATCTTTTGGTCCCGAGGCGCTCGGCATCGAATCTCTCAAGGA 457  
 Db 120 CAGTGGCAGTCACATCTTTTGGTCCCGAGGCGCTCGGCATCGAATCTCTCAAGGA 179

Qy 458 TTTCGGGTATACATCGAGGAGCTGAAGTCGGAGGAGAGACAGCTGCCAACACTGATTCTA 517  
 Db 180 TTTCGAGTATCTTCGGAGGAGCTGAAGTCGGAGGAGAGACAGCTGCCAACACTGATTCTA 239  
 Qy 518 AAGGATCCGAAGCAGCTCAACAGTACTTTCAAAAGACTGGAATGAATCTCAACCTTTC 577  
 Db 240 AAGGACCCCAACAGCTCAACAGCAGCTTCAGAGGACTGGAATGAATCTCAACCTTTC 299  
 Qy 578 CTGAATATGAATTTGAACGAGTATTTCCTAAAGTGTGCTCTTTTCCTTCATTAA 637  
 Db 300 CTGAATATGAATTTGAGAGGATTTCTTGAAGATGTCCTCTTCCTTCATTAA 359  
 Qy 638 ACAGAACCATTTACACCTCTTCTTTAGAACCGAG 677  
 Db 360 AATGAAGCAATTTACCTCTCTTCTTCAGACACGGG 399

## RESULT 9

## AL728651

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## BASE COUNT

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Mismatches

## Indels

## Gaps

## Qy

## Db

## Qy

## Db

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## Qy

## Db

QY 1065 TGGCGAGCTCTTCACTGTGATGTGGCGAAGCAAGCAAGAAATATATATACATT 1124  
 Db 263 TGGCGAGCTCTTCACTGTGATGTGGCGAAGCAAGCAAGAAATATATATACATT 322  
 QY 1125 TAGATGAAGAGAGCTCTGAGTCTTCCACATACATGAGCACTCCCAAGAGAGGCTCC 1184  
 Db 323 TGGAGAGAGAGCTCTGAGTCTTCCACATACATGAGCACTCCCAAGAGAGGCTCC 382  
 QY 1185 GGGCGGGCGAGGCTCTTCTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 1244  
 Db 393 GGGCGAGAGAGCTCTTCTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 442  
 QY 1245 TGGTCCAGCTTTTGGCGTCTTCTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 1304  
 Db 443 TCACTCCAGAGCTTGGCTCTTCTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 502  
 QY 1305 TGTGGGAGAGCTTCAAGCTCTGTAGAGAGGCGAGAGATGGGTATCCAGAGATCC 1364  
 Db 503 TGTGGGAGAGCTTCAAGCTCTGTAGAGAGGCGAGAGATGGGTATCCAGAGATCC 562  
 QY 1365 ACGAGTCCCGAGTTCATCTGTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 1424  
 Db 563 ACGAGTCCCGAGTTCATCTGTGTCTTCCAGTAAAGATGCGCAAGATCATCATGATG 622  
 QY 1425 AGACTACACACAAAG 1442  
 Db 623 GCCACCGAAGCAAG 640

RESULT 10  
 B0734807  
 LOCUS  
 DEFINITION AGENCOURT\_8510861 NICHID XGC Emb4 Xenopus laevis cDNA clone EST 16-JUL-2002  
 IMAGE:4684214 5', mRNA sequence.

ACCESSION B0734807  
 VERSION B0734807.1 GI:21873704  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

Xenopus laevis.  
 X. (bases 1 to 1010)  
 NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue procurement: Dr. Igor David  
 cDNA library Preparation: Life Technologies, Inc.  
 DNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: NCICGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.lnlni.gov/bbrp/image/image.html  
 Plate: LLAM10566 row: m column: 15  
 High quality sequence stop: 428.  
 Location/Qualifiers  
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 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:4684214"  
 /clone.lib="NICHID XGC Emb4"  
 /dev\_stage="embryo, stage 31-32"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site: 1;  
 Not; Site 2: SalI; Cloned unidirectionally. Primer: Oligo  
 3T. Average insert size 2.1 Kb. Constructed by Life  
 Technologies. Note: This is a Xenopus Gene Collection (XGC  
 ) library."

BASE COUNT 249 a 319 c 240 g 202 t  
 ORIGIN  
 FEATURES  
 source

Query Match: 12.63; Score 300.4; DB 14; Length 1010;  
 Best Local Similarity 70.38; Pred. No. 1: 5e-67;  
 Matches 443; Conservative 0; Mismatches 181; Indels 4; Gaps 3;  
 QY 825 ACTACAGCTCAACGACGAGGACCTTTTCAGCGAAGAGAGCTCTAGAGGAGGAGGAACTA 884  
 Db 19 ACTACAACTCAAGCAGAGGAGGCTCTTTAAACAGAGAGATCTCCGGAAGTGTGTAACA 78  
 QY 885 CAGAGAGACGACGCTGCTCTCTCAAAATGTCTTCCAGGGGATATATATATGAGCTGG 944  
 Db 79 CAGACTTCAACAACTGCTGATCCAGAGCTATCCCGGGGAGTATGTCATAGAGCTCG 138  
 QY 945 TGGATGACACTAAACACAAAGAAAGATGATGATGATGCTTTAAAGCCAGTGCATCTCC 1004  
 Db 139 TGAACACACACCAACAGCAGGAGCTTTCATGCTACTCTGCTGAAACCCAGTGCATCTCC 198  
 QY 1005 CGTGGCGCGCGCCATCAGAGCGCTGCCATCAGATGCCAGTGGCTAGTATCATATCGCAT 1064  
 Db 199 CTTGGCGCGCTCCATACAGAGCCATCGCCATTAAGTACCTGGTTCATATATCTGCT 258  
 QY 1065 TCGGAGAGCTCTTCTGCTGTGATGTGGCGAAGAGAGCAAGAAATATATATATTCACATT 1124  
 Db 259 TTGCCACTTTATTCACCGTCTATGTCCGCAAGAGCAGCAAGAAACATTTTACTCGCACC 318  
 QY 1125 TAGATGAAGAGAGCTCTGAGTCTTCCATCATGAGTGCACATGCCAGAGAGAGGCTCC 1184  
 Db 319 TGGACGAGGAGAGTTCGGAATCATCTACCTAGCGAGGAGTCTTCAGGTGGAGAGCCCC 378  
 QY 1185 GGGCGCGCGCGAAGGTCTTCTCTCTATTTCAGTAAAGATGCCAGATCATCATGATG 1244  
 Db 379 GCCCGCGCGCGAGTCTTCTCTCTACTCCACTCAAGATGTCAGAGCAGCATTAATG 438  
 QY 1245 TCGTCCAGTGTTCGCTCTCTCTCCAGGACTCTCTGCTGCTGA-GTGCTCTCGAC 1303  
 Db 439 TCATCCACTGCTTGGCTATTTCTGCTGAGATTTCTGTGGTGCCAGGGTTTCTGCTGAT 498  
 QY 1304 CTGTGGAGAGACTTCAAGCTCTCTAGAGAGGCGAGAGAGATGGGT-CATCCAGAGA 1361  
 Db 499 CTGTGGAGAGACTTCAAGCTCTCTAGAGAGGCGAGAGAGGCTTGGAGAGCAGAGA 558  
 QY 1362 TCCAGAGTCCAGTTCATCATTTGTGTTTGTTCAAAGGATATGAAGTACTTT-GTGGAC 1420  
 Db 559 TCCAGATTTCCCATCATCATCCATCGTCTGCCAGGCTCTCCAATACTTTGTGGTGCAC 618  
 QY 1421 AAGAGAGACTCAACACACAAAGAGGTG 1448  
 Db 619 AGAAAAAATGAAAGCCACAGGGGG 646

RESULT 11  
 AM646237  
 LOCUS  
 DEFINITION laevis cDNA clone PBK0161E05 5', mRNA sequence. EST 26-APR-2001  
 ACCESSION AM646237  
 VERSION AM646237.1 GI:7403719  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 Xenopus laevis.  
 X. (bases 1 to 485)  
 REFERENCE 1 (bases 1 to 485)  
 AUTHORS Blackhear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.C.,  
 Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman,  
 J.W., Bonaldo, M.F., and Soares, M.B.  
 The NIBS Maternal EST project: Interim analysis of the  
 first 13,879 ESTs from unfertilized eggs  
 Gene 267 (1), 71-87 (2001)  
 JOURNAL 21211403  
 MEDLINE  
 COMMENT Contact: Perry J. Blackshear  
 Office of Clinical Research and Laboratory of Signal Transduction











GenCore version 5.1.4\_p5\_4578  
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# OM protein protein search, using sw model

Run on: May 6, 2003, 13:34:21 ; Search time 43 Seconds  
(without alignments)  
2333.435 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWLCVSFTVNAQLNG ..... CKAIGCRSYDELHVAFL 753

Scoring table: BLOSUM62

Gapop 10.0 , Gapert 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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3:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4013	100.0	753	23	ABB07626
2	4003	99.8	753	23	ABB07627
3	3925	97.8	739	23	ABB07628
4	3901	97.2	738	22	AAU09904
5	3897	97.1	738	22	AAU09953
6	3896	97.1	738	22	AAU09954
7	3894	97.0	738	22	AAU09951
8	3894	97.0	738	22	AAU09952
9	3894	97.0	738	22	AAU09956
10	3890	96.9	738	22	AAU09955

11	3890	96.9	738	22	AAU09957	Human Interleukin
12	3830.5	95.5	738	23	AAU11355	Human DNA cytokin
13	3703	92.3	728	22	AAU04958	Human Interleukin
14	3703	92.3	739	22	AAU10602	Human Interleukin
15	3387	84.4	739	23	ABB07630	Murine cytokine re
16	2699.5	67.3	554	23	AAU91330	Human novel secret
17	1337	33.3	296	22	AAU10601	Human Interleukin
18	312	7.8	866	17	AAU04185	Human Interleukin
19	312	7.8	866	19	AAW61272	Human IL-17R prote
20	312	7.8	866	20	AAW92409	Human IL-17R prote
21	312	7.8	866	21	AAU99941	Human IL-17R prote
22	312	7.8	866	21	AAU97131	Human Interleukin
23	312	7.8	866	21	AAU97181	Human Interleukin
24	312	7.8	866	21	AAU03807	Human Interleukin
25	312	7.8	866	22	AAU62066	Human IL-17R (hCTL
26	312	7.8	866	22	AAU72754	Human Interleukin
27	306	7.6	864	17	AAU04184	Murine Interleukin
28	306	7.6	864	19	AAU61271	Mouse Interleukin
29	306	7.6	864	20	AAU92408	Murine IL-17R prot
30	306	7.6	864	21	AAU99935	Murine IL-17R prot
31	306	7.6	864	21	AAU97130	Murine Interleukin
32	306	7.6	864	21	AAU97180	Murine Interleukin
33	306	7.6	864	21	AAU03806	Murine IL-17R poly
34	306	7.6	864	22	AAU62060	Murine Interleukin
35	306	7.6	864	22	AAU72748	Murine Interleukin
36	271.5	6.8	539	23	AAU47457	Human IL-17 recept
37	135.5	3.4	238	20	AAU31624	Human IL-17RR matu
38	135.5	3.4	385	21	AAU25795	Human secreted pro
39	135.5	3.4	385	22	AAU75381	Human secreted pro
40	135.5	3.4	385	23	AAU47459	Human IL-17 recept
41	135.5	3.4	502	22	AAU29223	Human PRO polypept
42	135.5	3.4	502	22	AAU34349	Human EST encoded
43	135.5	3.4	502	22	AAU04955	Human Interleukin
44	135.5	3.4	502	22	AAU06586	Human protein havi
45	135.5	3.4	502	22	AAU87604	Human PRO5801. HO

## ALIGNMENTS

### RESULT 1

ABB07626  
ID ABB07626 standard; Protein; 753 AA.

AC ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

DE Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human; pulmonary alveolar proteinosis; familial periodic fever; antitumor; erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN WO200208259-A2.

PD 31-JAN-2002.

PR 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PR (ZYMO) ZYMOGENETICS INC.

PR Presnell SR, Kuestner RE, Gao Z;

PR WPI; 2002-217048/27.

PR N-PSDB; ABA95031, ABA95032.

PR New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor

growth, and modulating immune system by binding to endogenous zcytor18 ligand

Claim 1; Page 2; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 amino acid sequence.

Sequence 753 AA:

Query Match 100.0%; Score 4013; DB 23; Length 753;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWQLCSVFTVNAICNGSLVAAGSGRGADTCGPNKAAAPRLCVANEGVGP 60  
DB 1 MAPWQLCSVFTVNAICNGSLVAAGSGRGADTCGPNKAAAPRLCVANEGVGP 60

QY 61 ASRNLNITFYKDYNTYLPVGVKRVIAADQNTISQYACHQDVAVTILSPGALGIE 120  
DB 61 ASRNLNITFYKDYNTYLPVGVKRVIAADQNTISQYACHQDVAVTILSPGALGIE 120

QY 121 FLKGRVILELASEGRCQCCILKDPKQLNSFKRTGMESQPLNKKFTDVFYKVVVF 180  
DB 121 FLKGRVILELASEGRCQCCILKDPKQLNSFKRTGMESQPLNKKFTDVFYKVVVF 180

QY 181 PSIKNESNHPFFTRACDILLOPNLACKPFWKPRNLNLSQHSQDMQVSDPHAPNFG 240  
DB 181 PSIKNESNHPFFTRACDILLOPNLACKPFWKPRNLNLSQHSQDMQVSDPHAPNFG 240

QY 241 FRFFLVKLLKHEGPKRTCKQETTTSCLLQNVSGDYIELVDDTNTTRKVMHYA 300  
DB 241 FRFFLVKLLKHEGPKRTCKQETTTSCLLQNVSGDYIELVDDTNTTRKVMHYA 300

QY 301 LKPVHSPWAGIRAVAITVPLVVISAFATLFTVNCRRKQENIYSHLDEESSSTYTA 360  
DB 301 LKPVHSPWAGIRAVAITVPLVVISAFATLFTVNCRRKQENIYSHLDEESSSTYTA 360

QY 361 LPRRLRPFRKVELCYSSKDGQNNHNVVQCFAVFLQDFGCEVALDLDWDFSLCREGORE 420  
DB 361 LPRRLRPFRKVELCYSSKDGQNNHNVVQCFAVFLQDFGCEVALDLDWDFSLCREGORE 420

QY 421 WYIQIHESQFIIVCSGKMYVDKKNYKHGSGKGFELVAVSAIAEKLROAKQ 480  
DB 421 WYIQIHESQFIIVCSGKMYVDKKNYKHGSGKGFELVAVSAIAEKLROAKQ 480

QY 481 SSSAALSFATVDFSCSDVPGLDILSTKYRLMDNLPOLCSHLHSDRGHQEPQHTR 540  
DB 481 SSSAALSFATVDFSCSDVPGLDILSTKYRLMDNLPOLCSHLHSDRGHQEPQHTR 540

QY 541 QGSRNRYFRKSGRSLYVAICNMHOFIDEEPDMFKEQFVFPFPPPLRYEPVLEKFDGSL 600  
DB 541 QGSRNRYFRKSGRSLYVAICNMHOFIDEEPDMFKEQFVFPFPPPLRYEPVLEKFDGSL 600

QY 601 VLNDVCKPGPESDFCLKVEAAVILGATGPADSOHSGHGLDQDGEARPALDGSALQPL 660  
DB 601 VLNDVCKPGPESDFCLKVEAAVILGATGPADSOHSGHGLDQDGEARPALDGSALQPL 660

QY 661 LHTVACGSDMPRDSGLYDSSVSSLSLPLMEGLSTDTQETSSLTSSVSSSGLGEE 720  
DB 661 LHTVACGSDMPRDSGLYDSSVSSLSLPLMEGLSTDTQETSSLTSSVSSSGLGEE 720

QY 721 PPALPSKLLSSGSKADLCRSYTDLEHVAAPL 753  
DB 721 PPALPSKLLSSGSKADLCRSYTDLEHVAAPL 753

## RESULT 2

AB807627  
ID AB807627 standard; Protein; 753 AA.

XX AC AB807627;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 variant sequence.

XX KW Cytokine receptor; zcytor18; cell proliferative; antipsoriatic; human;  
XX KM pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
XX KM erythroleukemia; chromosome 3p14.3; gene therapy; variant.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 259 /label- T369M

XX FT FT /note- 'wild-type Thr is replaced with Met'

XX FT Misc-difference 750

XX FT FT /label- V750A

XX FT FT /note- 'wild-type Val is replaced with Ala'

XX PN WC200208259-A2.

XX XX 31-JAN-2002.

XX XX 23-JUL-2001; 2001WO-US23253.

XX XX 26-JUL-2000; 2000US-220747P.

XX XX (ZYMO ) ZYMOGENETICS INC.

XX XX Presnell SR, Kuestner RE, Gao Z;

XX XX WPI; 2002-217048/27.

XX XX N-PSDB; ABA95033, ABA95034.

XX PT New cytokine receptor polypeptide designated zcytor18, useful for  
XX PT inhibiting cell proliferation associated with psoriasis or tumor  
XX PT growth, and modulating immune system by binding to endogenous zcytor18  
XX PT ligand

XX PS Disclosure; Page 94-98; 119pp; English.

XX PS The invention relates to an isolated cytokine receptor polypeptide  
XX CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
XX CC standard recombinant methodology. The polypeptides can be used to inhibit  
XX CC cell proliferation associated with psoriasis or tumour growth. The  
XX CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
XX CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
XX CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
XX CC and localize zcytor18 gene expression in tissue samples. The probes are  
XX CC also useful for detecting gross aberrations in chromosome 3 in which  
XX CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
XX CC linkage-based testing of pulmonary alveolar proteinosis, familial  
XX CC periodic fever and erythroleukemia, and erythroleukemia associated with  
XX CC polymorphisms of cytokine receptors. The present sequence represents a  
XX CC human zcytor18 variant amino acid sequence.

XX SQ Sequence 753 AA;

Query Match 99.8%; Score 4003; DB 23; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPMLQLCSVFETVYACNGSLQAVAGSGRAGADTCGRMKAAARPRICVANEVGP 60  
 XX  
 DB 1 MAPMLQLCSVFETVYACNGSLQAVAGSGRAGADTCGRMKAAARPRICVANEVGP 60  
 QY 61 ASRNSGLNITFKYDNCCTTYLNPVGVKHVIAQAQNTISQYACHDOVAVTILSPGALGIE 120  
 DB 61 ASRNSGLNITFKYDNCCTTYLNPVGVKHVIAQAQNTISQYACHDOVAVTILSPGALGIE 120  
 QY 121 FLKGFVILEELKSEGRQCOOLILKDPKOLANSSFKRTGMSOPFLNMKFETDYKVVVPF 180  
 DB 121 FLKGFVILEELKSEGRQCOOLILKDPKOLANSSFKRTGMSOPFLNMKFETDYKVVVPF 180  
 QY 181 PSTKNSNTHPFFTRACDLLOPDNLACKPFRNPNLISQHGSDMVSQFSDHAPNFG 240  
 DB 181 PSTKNSNTHPFFTRACDLLOPDNLACKPFRNPNLISQHGSDMVSQFSDHAPNFG 240  
 QY 241 FRFYLHYLKLHKGPFKRTCKBOQTETTSCLLQNVSPGDYIIELVDDTNTTKVMHYA 300  
 DB 241 FRFYLHYLKLHKGPFKRTCKBOQTETTSCLLQNVSPGDYIIELVDDTNTTKVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQOENYSHLDEESSESYTAA 360  
 DB 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQOENYSHLDEESSESYTAA 360  
 QY 361 LPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420  
 DB 361 LPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420  
 QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRSGKGEFLVAVSAIAEKLROAKO 480  
 DB 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRSGKGEFLVAVSAIAEKLROAKO 480  
 QY 481 SSSAALSKFIATVYDSCGDVPGILDSTYRLMDNLPCLSHLRSHDGLQDPQOHTR 540  
 DB 481 SSSAALSKFIATVYDSCGDVPGILDSTYRLMDNLPCLSHLRSHDGLQDPQOHTR 540  
 QY 541 QGSRNYPFRSKGSLVAICNNHQFIDEEPDMFEKQFVFPHPPLRYREPVLKEDUSGL 600  
 DB 541 QGSRNYPFRSKGSLVAICNNHQFIDEEPDMFEKQFVFPHPPLRYREPVLKEDUSGL 600  
 QY 601 VLNDVCKPGPESDFCLKVEAAVLTGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660  
 DB 601 VLNDVCKPGPESDFCLKVEAAVLTGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660  
 QY 661 LHTVKAAGSPDMRDSGIYDSSVPSSELSLPLMBGLSTDTQETSSITSSVSSSSGLGEE 720  
 DB 661 LHTVKAAGSPDMRDSGIYDSSVPSSELSLPLMBGLSTDTQETSSITSSVSSSSGLGEE 720  
 QY 721 PPALPSKLLSSCGKADLCGRSTYDELHAAVPL 753  
 DB 721 PPALPSKLLSSCGKADLCGRSTYDELHAAVPL 753

## RESULT 3

ABB07628  
 ID ABB07628 standard; Protein; 739 AA.

XX AC ABB07628;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 splice variant.

XX KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;

XX KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;

XX KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

XX OS Homo sapiens.

XX PN W0200208259-A2.

XX PD 31-JAN-2002.

XX

23-JUL-2001; 2001NO-US23253.  
 26-JUL-2000; 2000US-220747P.  
 (ZYMO) ZYMOGENETICS INC.  
 Presnell SR, Kuestner RE, Gao Z;  
 WPI; 2002-217048/27.  
 N-PSDB; ABA95035, ABA95036.  
 New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.  
 Claim 1; Page 102-106; 119pp; English.  
 The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 splice variant.  
 Sequence. 739 AA;

Query Match 97.8%; Score 3925; DB 23; Length 739;  
 Best Local Similarity 98.1%; Pred. No. 0;  
 Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MAPMLQLCSVFETVYACNGSLQAVAGSGRAGADTCGRMKAAARPRICVANEVGP 60

DB 1 MAPMLQLCSVFETVYACNGSLQAVAGSGRAGADTCGRMKAAARPRICVANEVGP 60

QY 61 ASRNSGLNITFKYDNCCTTYLNPVGVKHVIAQAQNTISQYACHDOVAVTILSPGALGIE 120

DB 61 ASRNSGLNITFKYDNCCTTYLNPVGVKHVIAQAQNTISQYACHDOVAVTILSPGALGIE 120

QY 121 FLKGFVILEELKSEGRQCOOLILKDPKOLANSSFKRTGMSOPFLNMKFETDYKVVVPF 180

DB 121 FLKGFVILEELKSEGRQCOOLILKDPKOLANSSFKRTGMSOPFLNMKFETDYKVVVPF 180

QY 181 PSTKNSNTHPFFTRACDLLOPDNLACKPFRNPNLISQHGSDMVSQFSDHAPNFG 240

DB 181 PSTKNSNTHPFFTRACDLLOPDNLACKPFRNPNLISQHGSDMVSQFSDHAPNFG 240

QY 241 FRFYLHYLKLHKGPFKRTCKBOQTETTSCLLQNVSPGDYIIELVDDTNTTKVMHYA 300

DB 241 FRFYLHYLKLHKGPFKRTCKBOQTETTSCLLQNVSPGDYIIELVDDTNTTKVMHYA 300

QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQOENYSHLDEESSESYTAA 360

DB 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQOENYSHLDEESSESYTAA 360

QY 361 LPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420

DB 361 LPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420

QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRSGKGEFLVAVSAIAEKLROAKO 480

DB 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRSGKGEFLVAVSAIAEKLROAKO 480

QY 481 SSSAALSKFIATVYDSCGDVPGILDSTYRLMDNLPCLSHLRSHDGLQDPQOHTR 540

DB 481 SSSAALSKFIATVYDSCGDVPGILDSTYRLMDNLPCLSHLRSHDGLQDPQOHTR 540

Db 467 SSSAALSKFTAVFYDSCBGPVIGLIDLTSTYKRLMDNLPOLCSHLHSRDHGLQEPQHTR 526  
 QY 541 QGSRNRTFRKSGRSLYVAICNMHQFIDEPDFKQVPPHPPPLRYREPVLKFDGSL 600  
 Db 527 QGSRNRTFRKSGRSLYVAICNMHQFIDEPDFKQVPPHPPPLRYREPVLKFDGSL 586  
 QY 601 VLNDVCKPESDPCFLKVEAVLGATGPADSHQSHQGGIDQGEARPALDGSAAQLPL 660  
 Db 587 VLNDVCKPESDPCFLKVEAVLGATGPADSHQSHQGGIDQGEARPALDGSAAQLPL 646  
 QY 661 LHTVAGSPDMRDSGYDSSVSSLSPLMEGLSTDTSTSSVSSSGLGEE 720  
 Db 647 LHTVAGSPDMRDSGYDSSVSSLSPLMEGLSTDTSTSSVSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADGCRSYTDELHVAAPL 753  
 Db 707 PPALPSKLLSSGCKADGCRSYTDELHVAAPL 739

RESULT 4  
 AAU09904  
 ID AAU09904 standard; Protein: 738 AA.  
 AC AAU09904;  
 DT 14-FEB-2002 (first entry)  
 XX Human Interleukin 17 (hIL-17) receptor like protein.  
 DE Interleukin 17: hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.  
 XX Homo sapiens.  
 OS  
 XX WO200168859-A2.  
 PN  
 XX 20-SEP-2001.  
 PD  
 XX 15-MAR-2001; 2001WO-US06878.  
 PF  
 XX 16-MAR-2000; 2000US-189616P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX Jing S.  
 PI  
 XX WPI; 2001-611392/70.  
 DR N-PSDB; AAS15346.  
 DR  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma -  
 XX  
 PS Claim 2; Page 152-154; 150pp; English.  
 XX  
 PS The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rl) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal.

dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rl may also be used as  
 CC agents in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rl antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of the human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of  
 CC the invention.  
 XX  
 XX Sequence 738 AA;  
 Query Match 97.28; Score 3901; DB 22; Length 738;  
 Best Local Similarity 97.68; Pred. No. 0;  
 Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;  
 QY 1 MAPWLQCSVFTVACNLGSQLAVAGSGRARGADTCGRMKAAARPLCAVNEGVP 60  
 Db 1 MAPWLQCSVFTVACNLGSQLAVAGSGRARGADTCGRMKAAARPLCAVNEGVP 60  
 QY 61 ASRNSGLYNITEKYDNCCTTYLNPVGRHVIADQAQNTISQACHDOVAVTILMSPGALGIE 120  
 Db 47 ASRNSGLYNITEKYDNCCTTYLNPVGRHVIADQAQNTISQACHDOVAVTILMSPGALGIE 106  
 QY 121 FLKGRVYLEELKSGRCQQLIKDPKOLNSSFRKTMESQPLMKMETDYFVKVVPF 180  
 Db 107 FLKGRVYLEELKSGRCQQLIKDPKOLNSSFRKTMESQPLMKMETDYFVKVVPF 166  
 QY 181 PSKINSNHYEPFFETTRACDLILQPNLACKPKPKPNLILSQHSDMOVSFDHAPNFG 240  
 Db 167 PSKINSNHYEPFFETTRACDLILQPNLACKPKPKPNLILSQHSDMOVSFDHAPNFG 226  
 QY 241 FRFFYLHKHEGPKKTKCKEQTTTSCLLQNVSPGDIYIELVDNTNTRKWHYA 300  
 Db 227 FRFFYLHKHEGPKKTKCKEQTTTSCLLQNVSPGDIYIELVDNTNTRKWHYA 286  
 QY 301 LKPVHSPNAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESESESTYTA 360  
 Db 287 LKPVHSPNAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESESESTYTA 346  
 QY 361 LPRERLRPRKPVFLCYSSKQGNHNMVQCFAFLQDPGCEVALDLMEDFSLREGORE 420  
 Db 347 LPRERLRPRKPVFLCYSSKQGNHNMVQCFAFLQDPGCEVALDLMEDFSLREGORE 406  
 QY 421 WVTOKTHESQFIIVVCSKGMKYFVDKNTKHKGGSGSGKGFELFVAVSAEKLRAQK 480  
 Db 407 WVTOKTHESQFIIVVCSKGMKYFVDKNTKHKGGSGSGKGFELFVAVSAEKLRAQK 466  
 QY 481 SSSAALSKEIAVFDYDSCGDPVIGLIDLTSTYKRLMDNLPOLCSHLHSRDHGLQEPQHTR 540  
 Db 467 SSSAALSKEIAVFDYDSCGDPVIGLIDLTSTYKRLMDNLPOLCSHLHSRDHGLQEPQHTR 526  
 QY 541 QGSRNRTFRKSGRSLYVAICNMHQFIDEPDFKQVPPHPPPLRYREPVLKFDGSL 600  
 Db 527 QGSRNRTFRKSGRSLYVAICNMHQFIDEPDFKQVPPHPPPLRYREPVLKFDGSL 586  
 QY 601 VLNDVCKPESDPCFLKVEAVLGATGPADSHQSHQGGIDQGEARPALDGSAAQLPL 660  
 Db 587 VLNDVCKPESDPCFLKVEAVLGATGPADSHQSHQGGIDQGEARPALDGSAAQLPL 646  
 QY 661 LHTVAGSPDMRDSGYDSSVSSLSPLMEGLSTDTSTSSVSSSGLGEE 720  
 Db 647 LHTVAGSPDMRDSGYDSSVSSLSPLMEGLSTDTSTSSVSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADGCRSYTDELHVAAPL 752  
 XX



XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #4.  
 XX DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 XX mutin.

OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Misc-difference 374

XX /label- Val, Ile, Met, Leu, Phe, Ala, Nle  
 FT WO200168859-A2

XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.  
 XX Jing S;

XX WPI; 2001-611392/70.  
 DR Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma

XX Claim 21; Page -; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17p) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis and hypercalcaemia), myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17p may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17p antibodies and antagonists may also be used to down regulate  
 CC expression and activity.

CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 21.

XX Sequence 738 AA,  
 XX Query Match 97.1%; Score 3896; DB 22; Length 738;

Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPHLQCSVFTTACVCLNGSOLAVAGGSGRAGADTCGWRKMAARPLCVANEGVGP 60  
 DB 1 MAPHLQCSVFTTACVCLNGSOLAVAGGSGRAGADTCGWRKMAARPLCVANEGVGP 60  
 QY 61 ASRNGSLNITFYDNCCTTLPVGVKRVIAADQNTISQYACHQDVAVTILMSPGALGIE 120  
 DB 47 ASRNGSLNITFYDNCCTTLPVGVKRVIAADQNTISQYACHQDVAVTILMSPGALGIE 106  
 QY 121 FLKGRVILEELKSEGRQCQQLILKOPKQLNSFKRTGMSQPLPKMKETDIFYKVVVVF 180  
 DB 107 FLKGRVILEELKSEGRQCQQLILKOPKQLNSFKRTGMSQPLPKMKETDIFYKVVVVF 166  
 QY 181 PSIKNESNTHPFFTRACDLLOPONLACKPFKPRNLNISQSGDMQVSDHAPNFG 240  
 DB 167 PSIKNESNTHPFFTRACDLLOPONLACKPFKPRNLNISQSGDMQVSDHAPNFG 226  
 QY 241 FRFYLHYKLKHEGFKEKCKOFTTETSCLLQNVSPGDYIELVDSTNTTRKVMHYA 300  
 DB 227 FRFYLHYKLKHEGFKEKCKOFTTETSCLLQNVSPGDYIELVDSTNTTRKVMHYA 286  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQENIYSHLDEESSESTYTA 360  
 DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQENIYSHLDEESSESTYTA 346  
 QY 361 LPRERLRPRKPVFLCYSSKQGNHNVVQCFAFYFLQDFCGCEVALDLNEDFSLCREGORE 420  
 DB 347 LPRERLRPRKPVFLCYSSKQGNHNVVQCFAFYFLQDFCGCEVALDLNEDFSLCREGORE 406  
 QY 421 WYIQKTHESQFIIVVCSKGMKYFVKNNYKHGGGSGKGLFPLVAVSAIAEKLRQAKO 480  
 DB 407 WYIQKTHESQFIIVVCSKGMKYFVKNNYKHGGGSGKGLFPLVAVSAIAEKLRQAKO 466  
 QY 481 SSSAALSKPIANVYDCGVDGCIILDLSTKYLMDNLKPOLCSHLHSRHOGLRGOHTR 540  
 DB 467 SSSAALSKPIANVYDCGVDGCIILDLSTKYLMDNLKPOLCSHLHSRHOGLRGOHTR 526  
 QY 541 QGSRNRTFKSGRSLTYAICNKHOFIDSEPOWFEKQFPVPPHPPPLRYREPVLKFSGL 600  
 DB 527 QGSRNRTFKSGRSLTYAICNKHOFIDSEPOWFEKQFPVPPHPPPLRYREPVLKFSGL 586  
 QY 601 VLNDVMCKPQSPEDFCLKVEAVALGATGAPDSQHSQHSQHGGLDQDGEARPDGSAALQPL 660  
 DB 587 VLNDVMCKPQSPEDFCLKVEAVALGATGAPDSQHSQHSQHGGLDQDGEARPDGSAALQPL 646  
 QY 661 LHTVAKGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDDTETSSLTSSVSSSSGLGEE 720  
 DB 647 LHTVAKGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDDTETSSLTSSVSSSSGLGEE 706  
 QY 721 PPALPSKLLSSGSCADIGCRSYTDELHAPV 752  
 DB 707 PPALPSKLLSSGSCADIGCRSYTDELHAPV 738

## RESULT 7

AAU09951

ID AAU09951 standard; Protein; 738 AA.

XX AC

XX AAU09951;

XX DT 14-FEB-2002 (first entry)

XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #1.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;

XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

XX KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;

XX KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;

XX KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;

XX KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;

KW Interleukin 17 (IL-17) receptor like protein; immunomodulatory;  
 OS anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 OS Hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 FH anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 FT vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmologic;  
 FT hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 FN bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 PD munit. 220016859-A2.  
 XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-072460.  
 XX (AMGE-) ANGEN INC.  
 XX Jang, S.  
 XX WPI: 2001-611392/70.  
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma.  
 XX Claim 18; Page 7; 158pp; English.  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rip may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The  
 XX anti-IL17rip antibodies and antagonists may also be used to down regulate  
 XX expression and activity.  
 XX Note: This sequence is not given in the specification but is based on the  
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 XX and has been created according to information given in claim 18.  
 XX Sequence 738 AA:  
 Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPVLQCSVFETTYNACLSQSLAAGSGRGARGADTCGRMKAAARPRICLVANEGVGP 60  
 DB 1 MAPVLQCSVFETTYNACLSQSLAAGSGRGARGADTCGRMKAAARPRICLVANEGVGP 60  
 QY 61 ASRNSGLNITFKYDNCITTYLNPVGRHVIAQAQNTTISQYACHQDVAVTILWSPGALGIE 120  
 DB 47 ASRNSGLNITFKYDNCITTYLNPVGRHVIAQAQNTTISQYACHQDVAVTILWSPGALGIE 106

QY 121 FLKGRVILBELSEGRQCOQILKADPKQLNSSFKRTGMSQPLNKKEFTDYFKVYVF 180  
 DB 107 FLKGRVILEELSEGRQCOQILKADPKQLNSSFKRTGMSQPLNKKEFTDYFKVYVF 166  
 QY 181 PSIKNESNYHPFFFRTRACDLLLPDNLACKPFWKPRNLNISQHGSDQVYDFRAPHNG 240  
 DB 167 PSIKNESNYHPFFFRTRACDLLLPDNLACKPFWKPRNLNISQHGSDQVYDFRAPHNG 226  
 QY 241 FFFFLVHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIELVDOTNTTKVMHYA 300  
 DB 227 FFFFLVHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIELVDOTNTTKVMHYA 286  
 QY 301 LKPVHSPHAGPIRAVAITVPLVVISAPATLFTVWCKRKKOENITSHLDESSSSTYTA 360  
 DB 287 LKPVHSPHAGPIRAVAITVPLVVISAPATLFTVWCKRKKOENITSHLDESSSSTYTA 346  
 QY 361 LPRERLRPRKPVFLCYSSKDGQNHNVVQCFATFLQDFCGCEVALDLWEDFSLCREG 420  
 DB 347 LPRERLRPRKPVFLCYSSKDGQNHNVVQCFATFLQDFCGCEVALDLWEDFSLCREG 406  
 QY 421 WYIQIHESQPIIIVVCSKGMKYFYDKNKYKHGGGSGKGEFLVAVSAIAEKLRQAK 480  
 DB 407 WYIQIHESQPIIIVVCSKGMKYFYDKNKYKHGGGSGKGEFLVAVSAIAEKLRQAK 466  
 QY 481 SSSAALSXFIATFYDSCGDPVGLDLSTYKRLNDNLPLQCLSHLSRHDGLQEPQHT 540  
 DB 467 SSSAALSXFIATFYDSCGDPVGLDLSTYKRLNDNLPLQCLSHLSRHDGLQEPQHT 526  
 QY 541 QGSRNRYFRSKGSLVVAICNNHOFIDEPDMFEKQFVFPFPPPLRYREPVLKEDSG 600  
 DB 527 QGSRNRYFRSKGSLVVAICNNHOFIDEPDMFEKQFVFPFPPPLRYREPVLKEDSG 586  
 QY 601 VLNDVNCXPGPESDFCLKVEAVLCAATGAPADQSQHSQHGGLDQGEARPAIDGSAAL 660  
 DB 587 VLNDVNCXPGPESDFCLKVEAVLCAATGAPADQSQHSQHGGLDQGEARPAIDGSAAL 646  
 QY 661 LHTYKAGSPDMPRDSGIYDSSVPSSLSLPLMBGLSTDTQTTSLSLTSVSSSSGLGEE 720  
 DB 647 LHTYKAGSPDMPRDSGIYDSSVPSSLSLPLMBGLSTDTQTTSLSLTSVSSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADLACRSYTDDELHAPV 752  
 DB 707 PPALPSKLLSSGCKADLACRSYTDDELHAPV 738

## RESULT 8

AAU09952  
 ID AAU09952 standard; Protein; 738 AA.

AC AAU09952;

DT 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #2.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmologic;  
 XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 XX munit.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 227

XX /label= Phe, Leu, Val, Ile, Ala, Tyr

XX W020016859-A2.



XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Jing S.  
 XX WPI; 2001-611392/70.  
 Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 diabetes, psoriasis and glaucoma.  
 XX Claim 19; Page: 158pp; English.  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 receptor like polypeptides useful as vaccines and in gene therapy. These  
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 ophthalmological activities. The IL-17 receptor like nucleic acids and  
 proteins may be used to prevent and treat diseases associated with  
 inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
 include, for example, immune disorders (e.g. inflammation, diabetes and  
 transplant rejection), infections (e.g. hepatitis and septicemia),  
 weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 breast cancer), reproductive disorders (e.g. infertility and  
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 DNA and its complements may also be used as diagnostic probes to detect and  
 quantitate the presence of similar nucleic acids in samples and identify  
 patients needing restorative therapy. The IL17rp may also be used as  
 antigens in the production of antibodies against the proteins and in  
 assays to identify modulators of expression and activity. The  
 anti-IL17rp antibodies and antagonists may also be used to down regulate  
 expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 19.  
 XX Sequence 738 AA;

Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPWLCQSVFTVACVNGSLAVAGSGGARGADTCGRKAAARPLCVANEGVGP 60  
 DB 1 MAPWLCQSVFTVACVNGSLAVAGSGGARGADTCGRKAAARPLCVANEGVGP 46  
 QY 61 ASRNSGLNITFYKDYNTYLPVGVKHTADQNTISQYACHDQVAVTILWSPGALGIE 120  
 DB 47 ASRNSGLNITFYKDYNTYLPVGVKHTADQNTISQYACHDQVAVTILWSPGALGIE 106  
 QY 131 FLGKFRVILEELKSGRCQOOLIKDPKOLNSSFKRTGMSQPFNAKFTDYFKVVPVF 180  
 DB 107 FLGKFRVILEELKSGRCQOOLIKDPKOLNSSFKRTGMSQPFNAKFTDYFKVVPVF 166  
 QY 181 PSIKNESNTHPFFFTACDILLQPNLACKPFNKPRNLNISQSGDMQVSDHAPNFG 240  
 DB 167 PSIKNESNTHPFFFTACDILLQPNLACKPFNKPRNLNISQSGDMQVSDHAPNFG 226  
 QY 241 FRFFLYLKLKHEGFRKCKQBOTTTSCLLQNVSPGDYIELVDOTNTTRKHYA 300

DB 227 XRFYLYLKLKHEGFRKCKQBOTTTSCLLQNVSPGDYIELVDOTNTTRKHYA 286  
 QY 301 LKPVHSPWAGPIRAVAITVPLVISAFAITLVWCRKKQENIYSHLDESSSETTAA 360  
 DB 287 LKPVHSPWAGPIRAVAITVPLVISAFAITLVWCRKKQENIYSHLDESSSETTAA 346  
 QY 351 LPRERLRPRKVFVLCYSSKDGONHNVOCFAIFLDQFCCEVALDLWEDFSLCREGORE 420  
 DB 347 LPRERLRPRKVFVLCYSSKDGONHNVOCFAIFLDQFCCEVALDLWEDFSLCREGORE 406  
 QY 421 WYIOKIHESQFIIVVCSKGNKYFVDKKNYKHGGGSGKGEFLVAVSAIAEKLRAQK 480  
 DB 407 WYIOKIHESQFIIVVCSKGNKYFVDKKNYKHGGGSGKGEFLVAVSAIAEKLRAQK 466  
 QY 481 SSSAALSKEIAYFYDCEGDVPGILDLSTKYRLMDNLPLCASHLSRDHGLQBPQHTR 540  
 DB 467 SSSAALSKEIAYFYDCEGDVPGILDLSTKYRLMDNLPLCASHLSRDHGLQBPQHTR 526  
 QY 541 QGSRNRYFKSGRSIYVAICNHHQTIDEEPWFKEQVFPHPPIRYEPVLEKFSGL 600  
 DB 527 QGSRNRYFKSGRSIYVAICNHHQTIDEEPWFKEQVFPHPPIRYEPVLEKFSGL 586  
 QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAQPL 660  
 DB 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAQPL 646  
 QY 661 LRTYKAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTTSSLTSSVSSSGLGEE 720  
 DB 647 LRTYKAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTTSSLTSSVSSSGLGEE 706  
 QY 721 PPALPKLLSSGCKADIGCRSYTDELHAPV 752  
 DB 707 PPALPKLLSSGCKADIGCRSYTDELHAPV 738  
 RESULT 9  
 AAU09956  
 ID AAU09956 standard; Protein; 738 AA.  
 XX AC AAU09956;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.  
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 515 /label= Asp, Glu  
 XX PN W0200168859-A2.  
 XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.

PI Jing S;  
 XX WPI: 2001-611392/70.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX Claim 23; Page 7; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like-nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These  
 CC include, for example, immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17R may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17R antibodies and antagonists may also be used to down regulate  
 CC expression and activity.

CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 23.

XX SQ Sequence 738 AA;  
 Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

OY 1 MAPVLQCSVFTYVACGLNSQLAVAGSGRGACDTCGRKAAARPLCVANEGVGP 60  
 DB 1 MAPVLQCSVFTYVACGLNSQLAVAGSGRGACDTCGRKAAARPLCVANEGVGP 60  
 OY 61 ASRSLNLYNFKYDNTTYLNPVGRKHVIAQAQNTISQYACHDQVAVTILWSPGALGIE 120  
 DB 47 ASRSLNLYNFKYDNTTYLNPVGRKHVIAQAQNTISQYACHDQVAVTILWSPGALGIE 106  
 OY 121 FLGFRVILEELKSEGRCQCLILKDPQLNSSFRTGMSQPFLLNMFETDIYKVVVF 180  
 DB 107 FLGFRVILEELKSEGRCQCLILKDPQLNSSFRTGMSQPFLLNMFETDIYKVVVF 166  
 OY 181 PSTKNSYHFFETTRACDLLOPNLACKPFWKPNLINSQSGDMQVDFDHAPHNG 240  
 DB 167 PSTKNSYHFFETTRACDLLOPNLACKPFWKPNLINSQSGDMQVDFDHAPHNG 226  
 OY 241 FFETLHLYKLHKGFPFRKTKCKQETTTTSCLLQNVSPGDIILVDDTNTTRVNHYA 300  
 DB 227 FFETLHLYKLHKGFPFRKTKCKQETTTTSCLLQNVSPGDIILVDDTNTTRVNHYA 286  
 OY 301 LKPVHSPNAGITRAVATVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTVTA 360  
 DB 287 LKPVHSPNAGITRAVATVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTVTA 346  
 OY 361 LPERLRPRPKVFLCYCKSQGNHNVVQCFAYFLQDFCGCEVALDHEFSLCREGORE 420  
 DB 347 LPERLRPRPKVFLCYCKSQGNHNVVQCFAYFLQDFCGCEVALDHEFSLCREGORE 406

OY 421 WYQKHESQFIIVVCSKGMKYFDKKNYKHGGGSGSGKGBELFLVAVSAEKLRAQK 480  
 DB 407 WYQKHESQFIIVVCSKGMKYFDKKNYKHGGGSGSGKGBELFLVAVSAEKLRAQK 466  
 OY 481 SSSAALSFIAYFDYSCGDVPGILDLSTKYRLMDNLPLQCSHLSDHGLQSPGQHTR 540  
 DB 467 SSSAALSFIAYFDYSCGDVPGILDLSTKYRLMDNLPLQCSHLSDHGLQSPGQHTR 526  
 OY 541 QGSRNRYFRSGSLSLVAICNMHOFIDEEPDPPEKQFVFPFPPPLRYRREPLEKFDGSL 600  
 DB 527 QGSRNRYFRSGSLSLVAICNMHOFIDEEPDPPEKQFVFPFPPPLRYRREPLEKFDGSL 586  
 OY 601 VLNDVWCKPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQDGEAPALDGSALQPL 660  
 DB 587 VLNDVWCKPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQDGEAPALDGSALQPL 646  
 OY 661 LHTVWAGSPDMPDQSGIYDSSVPSSELSLPLMEGLSTDTTSTSLTSSVSSSGLGREE 720  
 DB 647 LHTVWAGSPDMPDQSGIYDSSVPSSELSLPLMEGLSTDTTSTSLTSSVSSSGLGREE 706  
 OY 721 PPALPSKLLSSGCKADLGCRTYDDELHAVAP 752  
 DB 707 PPALPSKLLSSGCKADLGCRTYDDELHAVAP 738

RESULT 10  
 AAU09955  
 ID AAU09955 standard; Protein; 738 AA.  
 XX  
 AC AAU09955;  
 XX  
 DT 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW muten.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 385 /Label- Cys, Ser, Ala  
 FT WO200168859-A2.  
 FN 20-SEP-2001.  
 PD 15-MAR-2001; 2001WO-US08678.  
 PF 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 FA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S;  
 DR WPI: 2001-611392/70.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX Claim 22; Page 7; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal lung dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17r may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17r antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22.

Sequence 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLCQSVFTVNAVLGSLAVAGGSGRAGCAGTCCGWRKAAARPLCVANEGVGP 60  
 DB 1 MAPWLCQSVFTVNAVLGSLAVAGGSGRAGCAGTCCGWRKAAARPLCVANEGVGP 46  
 QY 61 ASRNSGLNITFKYDNCYTLNPGKHVITADAGNTTISQACHQDVAVTILMSPGALGIE 120  
 DB 47 ASRNSGLNITFKYDNCYTLNPGKHVITADAGNTTISQACHQDVAVTILMSPGALGIE 106  
 QY 121 FLKGFVILEELKSGRCQOOLILKDPKOLNSFKRTGMSQPFLLMKFEEDYFKVVPF 180  
 DB 107 FLKGFVILEELKSGRCQOOLILKDPKOLNSFKRTGMSQPFLLMKFEEDYFKVVPF 166  
 QY 181 PSIKNESNTHPEFFTRACDLQLLPONLACKPFWKPRNLINSQSGDMQVSPDHAPNFG 240  
 DB 167 PSIKNESNTHPEFFTRACDLQLLPONLACKPFWKPRNLINSQSGDMQVSPDHAPNFG 226  
 QY 241 FRFFYLHYLKHGPFKTKCKQDQTTTSCLLQNVSPGDIIELVDDTNTTKVHYA 300  
 DB 227 FRFFYLHYLKHGPFKTKCKQDQTTTSCLLQNVSPGDIIELVDDTNTTKVHYA 286  
 QY 301 LKPVHFWAGPRAVAIVPLVLSAFATLFTVCRKQKQENIYSHLDESESESTYTA 360  
 DB 287 LKPVHFWAGPRAVAIVPLVLSAFATLFTVCRKQKQENIYSHLDESESESTYTA 346  
 QY 361 LPRERLRPKVFLCYSSKQGNHNVQCFAYFLQPCGCEVALDLMEDFSLCREQRE 420  
 DB 347 LPRERLRPKVFLCYSSKQGNHNVQCFAYFLQPCGCEVALDLMEDFSLCREQRE 406  
 QY 421 VWIOKIHESQFIIVCSKGMKIFVCKNKKHGGGSGKGFELFVAVSAIAEKLRQAK 480  
 DB 407 VWIOKIHESQFIIVCSKGMKIFVCKNKKHGGGSGKGFELFVAVSAIAEKLRQAK 466  
 QY 481 SSSAALSKEIAYFDYSCGVDVGLDLSTKYLMDNLPLQCSHLHSRHDHGLQPGQHT 540  
 DB 467 SSSAALSKEIAYFDYSCGVDVGLDLSTKYLMDNLPLQCSHLHSRHDHGLQPGQHT 526  
 QY 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDPSGL 600

DB 527 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDPSGL 586  
 QY 601 VLNDVWCKPSPEDCLKVEANVLGATGPAQDSQHSQHGGLDQGEARPDNGSALQPL 660  
 DB 587 VLNDVWCKPSPEDCLKVEANVLGATGPAQDSQHSQHGGLDQGEARPDNGSALQPL 646  
 QY 661 LHTVKAQSPDMRDSGYDSSVPSSELSLPLMBGLSTDDTSTSTSTSTSTSTSTSTSTST 720  
 DB 647 LHTVKAQSPDMRDSGYDSSVPSSELSLPLMBGLSTDDTSTSTSTSTSTSTSTSTSTST 706  
 QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPV 752  
 DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAPV 738

RESULT 11  
 AAU09957 standard; Protein; 738 AA.  
 XX AAU09957;  
 AC AAU09957;  
 DT 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.  
 XX  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 602 /label= Cys, Ala, Ser  
 FT Key Location/Qualifiers  
 PN WO200168859-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 15-MAR-2001; 2001WO-US08678.  
 XX  
 PR 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S;  
 XX  
 DR WPI; 2001-611392/70.  
 XX  
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX  
 PS Claim 24; Page -: 158pp; English.  
 XX  
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and

transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AA009904) and has been created according to information given in claim 24.

XX Sequence 738 AA:

Query Match 96.9%; Score 3890; DB 22; Length 738;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPQLQCSVFETVNAACLSQAVAGSGRAGADTCGRKAAARPRLCVANGVGP 60  
DB 1 MAPQLQCSVFETVNAACLSQAVAGSGRANGVTCGR -----GVGP 46  
QY 61 ASNSGLNITFKYDNTTTLNPKVGHVIAQAQNTISQYACHQDVAVTILWSPGALGIE 120  
DB 47 ASNSGLNITFKYDNTTTLNPKVGHVIAQAQNTISQYACHQDVAVTILWSPGALGIE 106  
QY 121 FLGPFVILEELKSGRCQQLLKDQKQNSFKRTGMSQPFLLNMFETDVFVKVVF 180  
DB 107 FLGPFVILEELKSGRCQQLLKDQKQNSFKRTGMSQPFLLNMFETDVFVKVVF 166  
QY 181 PSTKESNTHPFFTRACDLQLQDNLACKPFKPNLMSIQHSDMQVSDFHAPHNFG 240  
DB 167 PSTKESNTHPFFTRACDLQLQDNLACKPFKPNLMSIQHSDMQVSDFHAPHNFG 226  
QY 241 FRFYLHKLKHEGPKFKCKQEQTTTSCLLQNSPDYIIELVDDTNTTKVWHYA 300  
DB 227 FRFYLHKLKHEGPKFKCKQEQTTTSCLLQNSPDYIIELVDDTNTTKVWHYA 286  
QY 301 LAPVHSPNAGPRAVATVPLVVISAFATLVKCRKQENIKSHLDEESSSTYTA 360  
DB 287 LAPVHSPNAGPRAVATVPLVVISAFATLVKCRKQENIKSHLDEESSSTYTA 346  
QY 361 LPRERLRPRKVFCLYSSKQDQNNHNVQCFAYFLDFCCCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRKVFCLYSSKQDQNNHNVQCFAYFLDFCCCEVALDLWEDFSLCREGORE 406  
QY 421 WYQTKHESQITIVVCSKGMKVFQKKNYKKGGRGSGKGFELVAVSALAERLQAKQ 480  
DB 407 WYQTKHESQITIVVCSKGMKVFQKKNYKKGGRGSGKGFELVAVSALAERLQAKQ 466  
QY 481 SSSAALSFIAYFDYSCGDVPGILDSTKYRLMDNLQCLSHLSRDLGLOPQOHTR 540  
DB 467 SSSAALSFIAYFDYSCGDVPGILDSTKYRLMDNLQCLSHLSRDLGLOPQOHTR 526  
QY 541 QGSRNRYFRSNGSLVAICNHHQFIDEEPDMFEKQFVFPFPPPLRYREPVLKEDSGL 600  
DB 527 QGSRNRYFRSNGSLVAICNHHQFIDEEPDMFEKQFVFPFPPPLRYREPVLKEDSGL 586  
QY 601 VLNDVCKPSPESDFCLKVEAPVLGATGPADSOHESQHGGLDQDGCEARPDLDGSAALQPL 660  
DB 587 VLNDVCKPSPESDFCLKVEAPVLGATGPADSOHESQHGGLDQDGCEARPDLDGSAALQPL 646  
QY 661 LHTVAGSPDMPRDGIYDSSVPSSELSPLWELSLTDQTTSSITTSVSSSSGLGEE 720  
DB 647 LHTVAGSPDMPRDGIYDSSVPSSELSPLWELSLTDQTTSSITTSVSSSSGLGEE 706

QY 721 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 738

## RESULT 12

AAU11355  
ID AAU11355 standard; Protein; 738 AA.

XX AC AAU11355;

XX 26-MAR-2002 (first entry)

XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

XX Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;  
XX gene therapy; protein therapy; immunological disorder.

XX Homo sapiens.

XX Key: Location/Qualifiers

XX Misc-difference 25 /label= Val

XX FT /note= "Encoded by GTN"

XX WO200190358-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US16767.

XX 24-MAY-2000; 2000US-206862P.

XX (SCHE ) SCHERING CORP.

XX Gorman DM;

XX WPI; 2002-106198/14.

XX N-PSDB; AAS18134.

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.

Claim 1; Page 25; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8 polypeptide.

XX Sequence 738 AA;

Query Match 95.5%; Score 3830.5; DB 23; Length 738;

Best Local Similarity 96.3%; Pred. No. 0;

Matches 725; Conservative 2; Mismatches 11; Indels 15; Gaps 2;

QY 1 MAPQLQCSVFETVNAACLSQAVAGSGRAGADTCGRKAAARPRLCVANGVGP 60

DB 1 MAPQLQCSVFETVNAACLSQAVAGSGRAGADTCGRKAAARPRLCVANGVGP 46

QY 61 ASNSGLNITFKYDNTTTLNPKVGHVIAQAQNTISQYACHQDVAVTILWSPGALGIE 120



XX CC The sequence is PRO20026 which is the human Interleukin 17 receptor,  
 CC IL-17R4, encoded by DNA 154095-2998. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.  
 XX SQ Sequence 728 AA:

Query Match 92.3%; Score 3703; DB 22; Length 728;  
 Best Local Similarity 96.7%; Pred. No. 0;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RHKAARPLCYANE-GVGPASRSLNYITFKYDNCCTYLNPGVKHYIAQAQNTISQY 100  
 DB 3 RASAGVPALFVSGEGOGVGPASRSLNYITFKYDNCCTYLNPGVKHYIAQAQNTISQY 62

QY 101 ACHDOAVATILWSGALGIEFLAGFRVILELSEGRQCOOLILDKPOLANSSFKRGNE 160  
 DB 63 ACHDOAVATILWSGALGIEFLAGFRVILELSEGRQCOOLILDKPOLANSSFKRGNE 122

QY 161 SQFLNKKFETDYFKVVPVPSIKNESNTHFFTRACDOLLQPDNLACKPFWKPNLN 220  
 DB 123 SQFLNKKFETDYFKVVPVPSIKNESNTHFFTRACDOLLQPDNLACKPFWKPNLN 182

QY 221 ISO-----HGSQMVSDFAHPNFGFRFFLYHLKHEGPFKRTCKQBOIT 267  
 DB 183 ISQSGDMQVSDFAHPNFGFRFFLYHLKHEGPFKRTCKQBOIT 242

QY 268 ETTSCLLQNVSPGYIELVDVDTNTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 327  
 DB 243 EMTSCLLQNVSPGYIELVDVDTNTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 302

QY 328 ATLFTYMKCKQENIYSHLDESSSESTYTAALPRELRPRPKVFLCYSSKQGNMNV 387  
 DB 303 ATLFTYMKCKQENIYSHLDESSSESTYTAALPRELRPRPKVFLCYSSKQGNMNV 362

QY 388 VQCFATYFDGCGEVALDWEDESLCREGQREWIQIHESQFIIVVCSGKMYFYDKK 447  
 DB 363 VQCFATYFDGCGEVALDWEDESLCREGQREWIQIHESQFIIVVCSGKMYFYDKK 422

QY 448 NYRKHGGGRSGKGEFLVAVSAIAEKLQAKQSSAALSFKFTAVFYDSCGDPVGLD 507  
 DB 423 NYRKHGGGRSGKGEFLVAVSAIAEKLQAKQSSAALSFKFTAVFYDSCGDPVGLD 482

QY 508 LSTKYRLMDNLPOLCSHLHRSRDHGLQEPQHTROGSRNRYFRSKSRLYVAICNMQHFI 567  
 DB 483 LSTKYRLMDNLPOLCSHLHRSRDHGLQEPQHTROGSRNRYFRSKSRLYVAICNMQHFI 542

QY 568 DEPDNFKQFVPPHPPPLRYREPVLEKFDGLVNDVCKPGPESDCLKVEAAVLGAT 627  
 DB 543 DESPWFNFKQFVPPHPPPLRYREPVLEKFDGLVNDVCKPGPESDCLKVEAAVLGAT 602

QY 628 GPADSQHESQHGGLDQDGEARPAIDGSAALQPLLTHTYKAGSPDMDPSDGIYDSVSPSE 687  
 DB 603 GPADSQHESQHGGLDQDGEARPAIDGSAALQPLLTHTYKAGSPDMDPSDGIYDSVSPSE 662

QY 688 LSLPLMEGLSTDTQETSLTESVSSSGIGEEPPALPDKLLSSGSKADLCGRSYDEL 747  
 DB 663 LSLPLMEGLSTDTQETSLTESVSSSGIGEEPPALPDKLLSSGSKADLCGRSYDEL 722

QY 748 HAVAPL 753

DB 723 HAVAPL 728  
 RESULT 14  
 AAU10602  
 ID AAU10602 standard; Protein; 739 AA.  
 XX AAU10602;  
 AC AAU10602;  
 DT 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-1) receptor-like protein version 2.  
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmologic;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.  
 XX Homo sapiens.  
 OS  
 XX WO200168859-A2.  
 PN  
 XX 20-SEP-2001.  
 PD  
 XX 15-MAR-2001; 2001WO-US08678.  
 PE  
 XX 16-MAR-2000; 2000US-189816P.  
 PR  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX JIng S;  
 XX WPI; 2001-611392/70.  
 DR N-PSDB; AAS16201.  
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX Claim 2; Fig 1; 158pp; English.  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukaemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rlp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of

DE  
XX

матине сүтөккәне рецептор, зсүтөггя.

np

[illegible]

np







GenCore version 5.1.4\_p5-4578  
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OM protein - protein search using sw model

Run on: May 6, 2003, 13:41:01 ; Search time 48 seconds  
(without alignments)  
1508.109 Million cell updates/sec

Title: US-09-912-157-2  
Perfect score: 4013  
Sequence: 1 MAPWLQCSVEFTVNAQLNG.....CVALGCRSYDELHVAVAL 753

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_73:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3005	74.9	564	2 T42695	hypothetical prote
2	170.5	4.2	845	2 T27282	hypothetical prote
3	126.5	3.2	718	2 T30113	hypothetical prote
4	117	2.9	757	2 T03081	telomere-associate
5	117	2.9	917	2 T04661	hypothetical prote
6	117	2.9	2946	2 T00867	hypothetical prote
7	116.5	2.9	901	2 F83781	transposase (DB) /
8	115.5	2.9	938	2 T49071	protein kinase - m
9	115	2.9	998	2 S37627	protein-tyrosine k
10	110	2.7	535	2 T17212	hypothetical prote
11	110	2.7	592	2 T49239	vesicle transport
12	108.5	2.7	3788	2 T13960	beige protein homo
13	107.5	2.7	3942	2 T42730	Bassoon protein -
14	107	2.7	3788	2 T30851	lysosomal traffic
15	106.5	2.7	638	2 D86477	protein F1504.27 l
16	106	2.6	1448	2 A12007	Subtilase family p
17	105	2.6	901	2 T36093	dead finger nuclea
18	105	2.6	1571	2 T14155	zinc finger protei
19	104	2.6	1462	1 B36182	protein-tyrosine-p
20	103.5	2.6	663	2 A39897	GTPase-activating
21	103.5	2.6	930	2 A84668	Argonaute (AGO1)-1
22	102	2.5	813	2 B47485	ABR protein 2 - hu
23	102	2.5	859	2 A49307	98K GTPase-activat
24	101.5	2.5	822	2 A47485	ABR protein 1 - hu
25	101.5	2.5	1639	2 T50119	probable sensory t
26	101.5	2.5	641	2 T05497	hypothetical prote
27	101	2.5	664	2 T51247	ARR2 protein (impo
28	101	2.5	1275	2 A38985	nucleotide exchang
29	100.5	2.5	938	2 T05533	hypothetical prote

30	100.5	2.5	974	2 E59434	Rho GTPase activat
31	100.5	2.5	1007	2 T24643	hypothetical prote
32	99.5	2.5	657	2 E96949	serine/threonine p
33	99.5	2.5	794	2 S50069	213 protein - mous
34	99.5	2.5	981	1 F0HVGH	gag-abl polyprotei
35	99	2.5	341	2 H71716	190 kd antigen pre
36	99	2.5	783	2 A31491	sex-determining re
37	99	2.5	970	2 S63059	hypothetical prote
38	98.5	2.5	353	2 T33782	hypothetical prote
39	98.5	2.5	963	2 AD2381	type I site-specif
40	98.5	2.5	993	2 I48653	mouse developmenta
41	98.5	2.5	1050	2 G86582	exodeoxyribonuclea
42	98.5	2.5	1050	2 H72041	exodeoxyribonuclea
43	98.5	2.5	1050	2 C81624	hypothetical prote
44	98	2.4	526	2 T16124	hypothetical prote
45	98	2.4	820	2 S33794	hypothetical prote

ALIGNMENTS

RESULT 1

T42695  
hypothetical protein DKFp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C:Accession: T42695

R:Bioecker, H.; Boecker, M.; Brandt, P.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: 222230

A:Accession: T42695

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFp434N1928

C:Genetics:

A>Note: DKFp434N1928.1

Query Match 74.9% ; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8% ; Pred. No. 8.5e-234;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	190	HPFFETRADLLQPNLACKPFWKPRNLNISQHGSDMOVSFDHAPNFGFRFFYLHYK	249
DB	1	HPFFETRADLLQPNLACKPFWKPRNLNISQHGSDMOVSFDHAPNFGFRFFYLHYK	60
QY	250	LKHEGPFKRTCKQPTETSCILQNVSPGYIIELVDDTNTTRVWHYALKPVHSPWA	309
DB	61	LKHEGPFKRTCKQPTETSCILQNVSPGYIIELVDDTNTTRVWHYALKPVHSPWA	120
QY	310	GPTRAVAITVPLWISAFATLFTVMCKKQENIYSHLDESSESTYTAALPRERLPR	369
DB	121	GPTRAVAITVPLWISAFATLFTVMCKKQENIYSHLDESSESTYTAALPRERLPR	180
QY	370	PKVFLCYSSKQGNHNVVQCFAIFLQDFCGCEVALDIEDFSLCREGQREVIQKHES	429
DB	181	PKVFLCYSSKQGNHNVVQCFAIFLQDFCGCEVALDIEDFSLCREGQREVIQKHES	240
QY	430	QFTIVVCSKGMKYFYDKKNYKHKGSGKGEFLVAVSAIAEKLRQAKQSSAALSKE	489
DB	241	QFTIVVCSKGMKYFYDKKNYKHKGSGKGEFLVAVSAIAEKLRQAKQSSAALSKE	300
QY	490	IAYFYSCGQVPIILDSTKYRLMDNLPQLCSHLHSRQKGLQEPQHTROGSRNRYR	549
DB	301	IAYFYSCGQVPIILDSTKYRLMDNLPQLCSHLHSRQKGLQEPQHTROGSRNRYR	360
QY	550	SKSGRLYVAICNMHQFTDEDPQWFEKQFVPPHPPPLRYREPVLKEFDSGLVNDVMCKP	609
DB	361	SKSGRLYVAICNMHQFTDEDPQWFEKQFVPPHPPPLRYREPVLKEFDSGLVNDVMCKP	420
QY	610	GPESDFCLAEAAVLGATGPADSOHESQHGGLDQDGEARPALDCSAALQPLLTHTVKA	669

Db 421 GPESDFCLVPAAYVATGATGADSPADQSGHGLDQGEARPALDGSAAQLPLHTVKAQSP 480  
 QY 670 SDMPDSDGIDSSVPSELSLMBGLSTQDTSTSLTSSNSSSSGLGEEPPALPSKLL 729  
 Db 481 SDMPDSDGIDSSVPSELSLMBGLSTQDTSTSLTSSNSSSSGLGEEPPALPSKLL 540  
 QY 730 SSGCKADLGCGRSTDELHVAPL 753  
 Db 541 SSGCKADLGCGRSTDELHVAPL 564

RESULT 2  
 T27282  
 hypothetical protein Y64G10A.e - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T27282  
 R:Alnscough, R.  
 submitted to the EMBL Data Library, September 1999  
 A:Reference number: Z20336  
 A:Accession: T27282  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-846 <CH1>  
 A:Cross-references: EMBL:AL110498; PTDN:CAB54470.1; CESP:Y64G10A.e  
 A:Experimental source: clone Y64G10A  
 C:Genetics:  
 A:Gene: CESP:Y64G10A.e  
 A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e

Query Match 4.2%; Score 170.5; DB 2; Length 846;  
 Best Local Similarity 21.4%; Pred. No. 3.3e-05;  
 Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

QY 99 QYACHDOAVTILWSPGALGIFELKGRFVILELEKSEGRQCOQLLKDPQLANSFKRTG 158  
 Db 294 QY-CPEEYEVRLDSS--GIVMLQSAIITKDLRE-----IINRPPVQGEF----- 338

QY 159 MESQPLNMFEDYFVKVPPSPKSNESHFFPRACDQLLPDNLAC-KPFWKPR 217  
 Db 339 -----NFTDIEDLPLSPVPIESAHD-----GRC-LCVTENGSCSLADWKP 382

QY 218 NLNISQHSQMSQVDFDAPHNGRFFYLHYKLKHEGPKFKTKCBQTTTSCILLNV 277  
 Db 383 KLT-----RIEKPPATSN-----QTEESDGAEKDKREDTTWT----- 415

QY 278 SPGDYIELVDYDNTTRKVMH-YALKPVPSPMAGPIRAVAITVPLVVISAFATL--FTVM 334  
 Db 416 -----WHTYA-----ITGAIITAILFILSVCAGLCKYKF 445

QY 335 CRKQOENIYSHLDESSSTYTAALPRELRPRKPYFLCYSSKDGQNMNVVQCFAYF 394  
 Db 446 NKKKASNI--HLLENPAFS-HSGSIPL-ILKQISVLIYV-SHDSAQEAAYLAPFEL 500

QY 395 LQDFCGCEVALDWEFSLCRQGENVIOKIHESQFIIVCSGKMYFYDKNKNKHGG 454  
 Db 501 LNDVFNVLNVLWDDEDTI-ENRAETINSIVRANKVIILINSIG-AIF--RTVFRHQ- 555

QY 455 GRGSGKGLFLVAVSAIAEKLQAKQSSAALSFKFIYFYDSCGDV--PGILDSTKY 512  
 Db 556 -----EPAIERITGRND-----VIFDMOCELALQHPCVISCHFSY 591

QY 513-----RLMD-NLPQLCSHLHSRDLQEQOHTROGSRNRNFRSKSGRSIYVAI 560  
 Db 592 TNPKYVFPFPIINRLQVSIIP--NSLMTMTTALTEQAPPEQLAGFNQVFAR---LQAAI 644

QY 561 CMNHQFIDEEDPFER-----QVPPHPPPLRYR----- 589  
 Db 645 SRKLANIESDQFQFETHUKVATRVSELAHNIVPL-PPGLEVKVVEDEDAQGMETLPI 703

QY 590 EPVLEKFP-----DSGLVNDVMCKPGPESDFCLVPAAYVATGATGADSPADQSHES 636

Db 704 DELKEKFAAKRQLEVEDLSDVRLLEDVKECAPGP-----IHVETPEVLEPASEPME 758  
 QY 637 QHGGLDQDGEARPALDGSAA--LQPLL-HTVKAGSPDMPDSDGIDSSVPSELS 689  
 Db 759 ARED-EDEDVDSVGGTARIEELQRLIVH-----KDNHDSGNLDSAYVSGSDFS 809

RESULT 3  
 T30113  
 hypothetical protein F56D1.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T30113  
 R:Chissos, S.; Wilson, R.  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid F56D1.  
 A:Reference number: Z20737  
 A:Accession: T30113  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-718 <CH1>  
 A:Cross-references: EMBL:U39997; PTDN:AAA81100.1; CESP:F56D1.2  
 C:Genetics:  
 A:Gene: CESP:F56D1.2  
 A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2

Query Match 3.2%; Score 126.5; DB 2; Length 718;  
 Best Local Similarity 21.1%; Pred. No. 0.091;  
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

QY 363 RERLRPRP-----KVFLCYSSKDGQNMNVVQCFAYFLQDFCGCEVALDWEDES 412  
 Db 398 RDKVRSREVNIALTEFVKVIVTAD-DNDLHTDCVKLVENLANCSCDPVDFLEKIT 456

QY 413 LCRCOREWVIOKIHESQFIIVCSGKMYFYDKNKNKHGGSGKGLFLVAVSAIA 472  
 Db 457 AEQVPSRWLVDDISLKRFLIIVSDCAEKILDTSEASETHQVQARPPADLGPANEMI- 515

QY 473 EKLQAKQSSAALSFKFIYFYDSCGDV--GILDSTKYRLMDNLPQLCSHLHSRD 539  
 Db 516 --IRDATHNPEARKKYAVRVFNTS--PHVPPNLAAILNLT-FILPEQFAQLTAFLHVE 570

QY 530 HGLAEPQOHTROGSRNRNFRSKSGRSLY--VAICNMHQFTDEDPWFKEQVFP----- 580  
 Db 571 H-----TERANVTONISEAQIHEWNLCSRMMSFFVRNPNNLETRMKPKDELA 619

QY 581 FHPPLRYRPPVLEKFDGSLVNDVMCKPGPESDFCLVPAAYVATGATGADSPADQSHES 640  
 Db 620 LH---LAKQSPVIVPIQT-----EED--RIASIKYLVPPQALVDSO--- 657

QY 641 LDQGEARPALDGSAAQLPLHTVKAQSPDM--PRDSGIYDSSVPSELSLPLMEGLST 698  
 Db 658 -DED-----DVLQDP--HASHQNPILLPLPEQCG-----PDSO-----SD 690

QY 699 DQTTTSLTSSVSSSSGLGEEPPALPSK 727  
 Db 691 SESDSSSESESDNEG---EDPKTIIVVK 716

RESULT 4  
 T09081  
 telomere-associated recQ-like helicase - smut fungus (Ustilago maydis) (fragment)  
 C:Species: Ustilago maydis (corn smut)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-May-2000  
 C:Accession: T09081  
 R:Sanchez-Alonso, P.; Guzmán, P.  
 Genetics 148, 1043-1054 1998  
 A:Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motif  
 A:Reference number: Z16557; MUID:98198830; PMID:9535423  
 A:Accession: T09081  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A:Residues: 1-757 <SN>  
 A:Cross-references: EMBL:AF030885; NID:92642221; PID:92642222  
 A:Experimental source: strain FB2  
 C:Genetics: 72  
 A:Gene: UTASreco  
 C:Keywords: DNA binding

Query Match: 2.9%; Score 117; DB 2; Length 757;  
 Best Local Similarity: 20.4%; Pred. No. 0.57;  
 Matches: 111; Conservative: 56; Mismatches: 187; Indels: 190; Gaps: 27;

QY 268 ETTICLQNTSPGDIYIELVDVNTTRKVMHVALKPVHSPWAGPIRAV---AIVPL-- 321  
 DB 77 ETTILLPTVALRANNAKLDMH---IRYHWQP-GSKAAPIVLVSTEAATLAKKE 131  
 QY 322 ---VLSAFATLPTVWCKKKQENIYSHLDESSESTTAALP----- 362  
 DB 132 YANRLQQQLRIVIDCHLTLPARSYRSMQLANHVRVETQVMTLTPPLPFDPA 191  
 QY 363 ---REKLAPRKVF-----LCYSSKDGONHNVVQCF-AIFLQDFGCEVALDNEDF 411  
 DB 192 FISHMKTLPLIVRESTNRSNLCYSVTAERHNSGHTCYDAVYVD--ECRARTDIW--- 246  
 QY 412 SLICREGQRENVVIOKIHESQFIVVCSKGMKFFYDK-----KNYKHKGGGRGS----- 458  
 DB 247 ---NGORD-----RIIVYCTS--KELVARLAEMLCGAAYSSSESEADKAAIIQ 290  
 QY 459 ---GKELFLVAVSAIAEKLRQAKQSSAALSKEFIATVFDYSCGDPGIL--DLSTKY 512  
 DB 291 DWICGKSPVIVATSA-----LVGVFDYPHVRVTHLLQPDLLTDF 331  
 QY 513 ---RLADMLPOLCSHLHSRDHGLQDFGQHTQGRSRNRYPS 550  
 DB 332 SQESGRAGRGCPAESILLQGLDDRAP--ASGKASSAEKGVAPG---ADREMAQLYRS 387  
 QY 551 KSGSLVAVICNNHQITDEEDPNEKQFVFPHPPLRYREPVELEKFDGLVNDVNCXPG 610  
 DB 388 RK---YCLRGVLSQLIDQSDW-----RWCMEGDQLCSVC 419  
 QY 611 PESDFCLKVEAAYLGTATGADSOH---ESQHGQLDQDGARPALDGSAAQLPLATVRAG 667  
 DB 420 PGHIF-----QARGPGQGFHTAPAQAGDPSTQGRHPSHGSS--HPSMH----- 463  
 QY 668 SPSDMPRDSGIYDSVPSE--LSLPLMEGLSTDTQETSLTESYSSS---SGLGEEPPA 723  
 DB 464 ---GSSHPSHGSSHPISGSHSHTGSS--HPSINGSGQGGGRRKQKQPD 510  
 QY 724 LPSK 727  
 DB 511 PPSE 514

RESULT 5  
 T04661  
 hypothetical protein F8D20.70 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision-23-Apr-1999 #text\_change 24-Nov-1999  
 C:Accession: T04661  
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,  
 submitted to the Protein Sequence Database, July 1998  
 A:Reference number: 215381  
 A:Accession: T04661  
 A:Molecule type: DNA  
 A:Residues: 1-917 <BE>  
 A:Cross-references: EMBL:AL031135  
 A:Experimental source: cultivar Columbia; BAC clone F8D20  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685/3  
 A:Note: F8D20.70  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match

2.9%; Score 117; DB 2; Length 917;

Best Local Similarity: 18.3%; Pred. No. 0.76; Mismatches: 130; Indels: 320; Gaps: 42;  
 Matches: 167; Conservative: 130; Mismatches: 296; Indels: 320; Gaps: 42;  
 QY 19 NGQLAVAGGSGRARGADTCGRW--KAAARPR-----LCVANEGV----- 58  
 DB 92 NGRSVSV-----GYSG--DILINSIFSGKGCSPSSAMICKLNLGKSEKIPDIASLAWY 145  
 QY 59 --GPASR-----NSGLNITFFYDNCITTLAPVGHV---IADAQNI--TISOVACHDQ 105  
 DB 146 AGRKASRVVIGSSNSIQVLLNEOTETRMILKGLHVSEPCADMEMIADYNEQSKHKQ 205  
 QY 106 VAVTILWSPGALGI--EFLKGFVLEELKSBGRCQOLIKDPKOLNSFKRTGMSOP 163  
 DB 206 DFLVGLKSGRVAYDDVMIEKYLIOSSKSSPSLPKVTWVLPFPSSSITVGFETNP 265  
 QY 164 ---FLMKFFETDY-----FYKVVPFSSIKNSN---YHPFP-----FTTRCDLLLOPD 206  
 DB 266 SHLLNLSDE--DTAQLAKADAVPFLPFTVFKSSRSRSHGPGTKVKNVITIGHCOTISW 324  
 QY 207 NLACK-----PFWKPR--NLNISOHG-----SDMOVSFDHAPNFGFFLYHY 248  
 DB 325 DMTCSFPIVLFLKEQIDQDYSSRGNALTAHLHYOSNRLVSGDNGHVRLYREKPEPY 384  
 QY 249 KLKH-----EGPFKR-----KTCQEQTTTETTCLLQNVSP-----GDYIIELV 287  
 DB 385 LTENSFTPGGSLKGNHIVQSVKYTKLTGTSITCIQKSNRHLAIGSDQGHDSLVEVI 444  
 QY 288 DDTWTRKVMHVALKPVHSPWAGPIRAVAVITVPLVVISAFATLPT----- 332  
 DB 445 D-----ALTPVY-----LVSLVDIEEANNVLYTKHIASDICPGIISLQ 482  
 QY 333 ---VCKKKQENIYSHLDESSESTTAALPRELRPRPKVFLCYSSKD 380  
 DB 483 FESCIVOGTEKVLVAVARDSSVFA--LDSDTGMNIGTNNIKPK-----APFVLTWQILD 536  
 QY 381 GQNNNVVQCFAYFAYLQDFGCEVALDNEDFSLCREGQRENVVIOKIHESQFIVVCS--- 437  
 DB 537 GK-----ODTSG-----NGFOTSRES-----TVEEISIFQPSVLVCSKA 571  
 QY 438 ---KGMKYFVDKKNYRHKG-----QGRSGKGEFLVAVSAIAE-----K 474  
 DB 572 IYIYSLARVVGQVKVLKHKKSSPICSSASTFYTGSGV--LTLVFTDGTVEIRSLPE 628  
 QY 475 LROAKQS-----SSAALSNAFIATVFDYSCGD-----VPGILDLSKYRLMD 516  
 DB 629 LSQLKQTSIRGTYSPPKPNLSPEITISASWDGDLVWVNGDDELIVSSVLPKQETFLVE 688  
 QY 517 NLPOLCSHLHSRDHGLQDFGQHTQGRSR-----NYFRSESGSLYVAICNMHOFIDEE 570  
 DB 689 SN-----NRVYKDNQSVCHEGIIITSSPREKKSVMFGSVFKRSKRTDTDPESKKTIEEL 744  
 QY 571 PDWFERQFVPF-----HPPPLRYRPPVLEKFD 598  
 DB 745 SKIFSTANFPNNNNVNSREINTITRVEDEEELDDIDDIDHHPNQOQKPKQEGTLS 804  
 QY 599 GL-----VLNDVMCKPGSDPCLVAAVILGATGPADSOHESQHGGL----- 641  
 DB 805 GLSKQKMANRFSNFKGLQKMAAANKRSVV---TNDEKHEEKNGATVDQIKKKYGTSS 860  
 QY 642 DQDCARPALDCAALQPLLTHTVKGSPDMPRDSGIYDSVPSSSELSPLMEGLSTQDT 701  
 DB 861 DEMAANKA-----QSKLQD-----NLKKLGISLRTT 888  
 QY 702 ETSSITSESVSSS 714  
 DB 889 EMDTAKSFSSSTA 901

RESULT 6  
 T00867

hypothetical protein At2g45540 [Imported] - Arabidopsis thaliana  
 N:Alternate names: hypothetical protein F17K2.7  
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 sequence\_revision 12-Feb-1999 #text\_change 16-Feb-2001

C/Accession: T00867; G84891

R/Author: S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, March 1998

A/Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.

A/Reference number: 214207

A/Accession: T00867;

A/Status: translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-2946 <R0U>

A/Cross-references: EMBL:AC003680; NID:92979540; PID:92979554

A/Experimental source: Cultivar Columbia

R/Lin: X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Zilberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617157

A/Accession: G84891

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2946 <SFO>

A/Cross-references: GB:AE002093; NID:92979554; PID:AC06163.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

A/Introns: 652/1; 913/3; 1165/3; 1210/3; 1245/3; 1283/3; 1309/2; 1336/3; 1438/3; 1638/2;

; 2449/2; 2481/3; 2643/1; 2890/3; 2931/3

Query Match 2.9%; Score 117; DB 2; Length 2946;

Best Local Similarity 18.7%; Pred. No. 4.3;

Matches 164; Conservative 105; Mismatches 314; Indels 294; Gaps 40;

QY 2 APWLCSEVFTVACLSGSLAAAGSGRGAGDTCGRWKAARPRCLVANEVCGA 61

DB 393 ATWIVIESFADTLNAATAAATAA---AKSGTSAMSAANAAS---ALAGEC--- 441

QY 62 SRNSGLNITFKYDCTYLPVGHVIAADQNTISQACHQDVAVTILMSPGALGIEF 121

DB 442 ---FAHPRLEFSLDNOQIEAFHA--- ---QF 467

QY 122 LKGFVILEELKSGR--- ---QC--- ---QQLILKPKOLNSSFKRTG 158

DB 468 L---VVESSGGRKSSLFHFAKPKQWYFGLHSCQGLLGRAESELRLYIDGSL 522

QY 159 MESQPLANKPEETDYFKVVPFSPKSNHYHPFF--- ---RTRACDLL 202

DB 523 YESRPF--- ---DPRISK--- ---PLSFCCIGTNPPTNAGLQRRRCPLF 563

QY 203 LO---PDNLACKPFWKPNLNISQSDMNOVSFOHAPNFGFRFFVLYKLKHGEPFKRT 260

DB 564 AEMGPYIFKEPIGPERMARLASRGDVLPCFNGA---GLFWLATNDYVN--- 612

QY 261 CROQTETTS--- ---CLLQNVSPGDYIELVDNDTNRK--- ---VMHYA--- 300

DB 613 -KAESSILDAIGYTHLYHPCLLSGRFCPD---ASLSGAAGTLRRPAEVLQGVHATR 669

QY 301 LKPVHSPNA--- ---GPIRAVATV--- ---PLVVISAPATLETVM--- 334

DB 670 MKPVESFVALAAGPMNLLPLVSSVHKDSLPCGLNPLSLSTVTTLAAPVRIMSAIQ 729

QY 335 --- ---CRKQOE--- ---NTYSHLDEESSESTYTAALPRELRPRKVFICYSKDGON 383

DB 730 HPGNNEELCRQGPILARILSYLLHSLASLORHGVGEEL---VAATVSLCQSQK---IN 786

QY 384 HNNVQCAFAFLQDCCEVALDHEFSLCREGQEWYIWKHESQFIIVVCSKHK--- 441

DB 787 HVLKQLFETILLD--- ---LKN--- ---SLCNYGLQKLLSSLDQNVFETATAMOREAI 836

QY 442 --- ---YFVDKKN--- ---YKHGGRGSGKGEFLFVAVSATAEKLROAKQSSAA- 485

DB 837 QLLDGCRCRYWMISEKDSFTFFLDGNTROMGELNALIDELVITIELLAGAASPSLAAD 896

QY 486 -LSKFIANYFYSCGDVPGILDITKVRMLDNL---POLCSHLHSRDBGLQE---PQOH 538

DB 897 DLRLGLGFIIDSPQPNQVAVRVLHLMATRVVOPNAARQMFQAEVFTSGGIETLLVLLQRE 956

QY 539 TROGSRNRYFRKSGSLVAICNNHOFIDEEPWFKEQVFPFPPPLRYRVPVLEKFS 598

DB 957 AKTGEDNYLWNGRSGKR--- ---SSTDPSKRS---PIN--- ---ESGSVKQLDS 995

QY 599 GLVLNDV-MCKPGPESDFCLKVEAAVLGATG-PADSQHESQHGGLDQGEARPDALGSAA 656

DB 996 NPHDNEIGFDLPGPGDGN---SVEDDNGVSGLNVPESVRQKEHG--- 1035

QY 657 LQPLHRTVKAGSDMRDPSGYDSSVPSSELSLPLMKGSLTQOTETSSLTSSVSSGL 716

DB 1036 --- ---STPVWCSDSVSISNIFERLS--- ---AETGGISLSISADSAR 1074

QY 717 GE--- ---EPPA--- ---LPSKLLSSGSCADLGCRS 742

DB 1075 NNIVNDNSDAVVVGIIIRLIGALISSGHLTFDFDARS 1111

RESULT 7

F83781

transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] --Bacillus

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C/Accession: F83781

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: F83781

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-301 <SFO>

A/Cross-references: GB:AP001510; GB:BA000004; NID:910173440; PIDN:BA04773.1; GSPDB:G

C/Experimental source: strain C-125

C/Genetics:

A/Gene: BH1054

Query Match 2.9%; Score 116.5; DB 2; Length 901;

Best Local Similarity 19.6%; Pred. No. 0.82;

Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 61 ASRNSGLNITFKYDCTYLPVGHVIAADQNTISQACHQDVAVTILMSPGALGI 119

DB 333 ALKESGL--- ---PLPKTLIADAGYSGESNYVRADELCTCTGS--- 371

QY 120 EPLKGFVILEELKSGR--- ---QCOQL--- ---ILKDPKOLNSSFKRTGHSOPFLANKF 169

DB 372 ---HTFR---QBQKRSFAKRHPYINRCDETDVYPCPNKRVSKFRITRTDPI---GT 423

QY 170 ETDYFV--- ---KVFPF-PSI--- ---KNESNYHFFFRTRACDILLQPDMLACKPFWKPR 217

DB 424 ARDFKVEYECESGCFPECKTAKGRNQRVYHPVY--- ---EELAKQHOKLK 471

QY 218 NLNISOHQ--- ---SDMOVSDHAPNFGFRFFVLYKLKHGEPFKRTCKEQOTTET 269

DB 472 ---SEEGRTLYOKRKTDESVEFGHVQNGLQFRRLHRLGK--- --- 507

QY 270 TSCLLQNVSPGDYIELVDNDTNRKVMHVALKPVHSGPWAGPIRAVAITVPLVVIS-AFA 328

DB 508 --- --- --- --- ---ESVHIELGLVALAHNL 524

QY 329 TLFTVACKKKQENIYSHLDEESSESTYTAALPRELRPRKVFICYSKDGONHNVY 388

DB 525 KRATVDRKSEKPNANTQHKNNR--- --- --- ---RIKRP--- ---SREYVL 558

QY 389 QCF--- ---AYFLQDCCEVALDHEFSLCREGQEWV--- ---YKHESQFIIVVCSKHK 441

DB 559 RCFWDSPEFKSDQKQYASFALED--- ---KLREGGNNIEVILDSKTYNRQV--- ---KGIN 612

QY 442 YFVDKKNYKHGGRGSGKGEFLFVAVSAI--- --- --- ---AEKLQAKQSSAALS 488

Db 613 MFTEKGVGLGPNAGKTTSMISLIQPTSGDVLKGGSIHKQSKAIRSLGVVPO 672  
 QY 489 FIAYDYCE---GDVPGTLDLSTKYLMDNLPQLCSHLHSDRGHQAEPQHTROG 542  
 Db 673 EIAVYHDLTARENLAFTKYGKLGKELKHR-MESTIQLV-GLBE-----RON 718  
 QY 543 SRNYSKRSKRSIYVAICNNHQ---FIDEEP 571  
 Db 719 DRVHTSGMKRLNIAVALLHPELIIDWP 750

## RESULT 8

149071 protein kinase - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: I49071  
 R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.  
 Mech. Dev. 48, 153-164, 1994  
 A:Title: Identification of novel protein kinases expressed in the myocardium of the developing mouse embryo  
 A:Reference number: I49071; MUID:95200798; PMID:7893599  
 A:Accession: I49071  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-938 <RES>  
 A:Cross-references: EMBL:U11493; NID:G595418; PIDN:AA67925.1; PID:G595419  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; transmembrane protein  
 F:571-839/Domain: protein kinase homology <KIN>  
 F:579-587/Region: protein kinase ATP-binding motif  
 F:862-928/Domain: SAM homology <SAM>

Query Match 2.94; Score 115.5; DB 2; Length 938;  
 Best Local Similarity 19.04; Pred. No. 1;  
 Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFTFVNAQL-NGSOLAVA---AGSGR---ARGADTCGRWKAARPRLC----- 52  
 Db 170 SLVIAFRACIANAVEVSLPKLYCNGDGMVPGACTCATGHEPAKESOCACPPGSI 229  
 QY 53 VANEVGVA-----SRNSG-----LYNITEKVDN-----CTTILNPVGRHVIADAO 93  
 Db 230 KAKQGEPCPCPNNSRTTSPASICTCHNFEYRADSDSADACTIRSP-PROVISNV- 287  
 QY 94 NITISYACHQDVAVILMS-PGALGIEFLKGRVILEELK-SEG-----RCCQILIL 144  
 Db 288 -----NETSLILENSEPRDLGGDDLLYNVICKKRGSGGAGGATCSCDDNVE 337  
 QY 145 KDPKQLNSFKRTGSESQPLLNKFFETDYFVYVPPFSPKNSNYHPFFETTRACDILLQ 204  
 Db 338 FVPRQLGLTRRVHIS-----HLLAHTRYTEVQAVNGSGKSPPLPRYAAVNTTNOAA 392  
 QY 205 PDNLACKPMPKRNILNSQSGDMOVSDPHAPNFGPRFFLYLKLKHEGPF-KRKTCKQ 263  
 Db 393 PSEV-----PTLHSUSTSGSLTSLNAPPERNG---VILDYEMKY---FEKSKAIAS 439  
 QY 264 EQTTETSCLLQNVSP-GDYIIELVDDTNTTKY-----MHALKPVHSWAGPIRAVA 316  
 Db 440 TVTSQKNSVOLDGLOPOARYVVOV-----RARTVAGYQYTHPAEFETTSERGSQAOLQ 494  
 QY 317 ITYPLVVISAFSA-----TLTVNCRKQKQENIYSHLDEESSSTVTAALPRERLRP 368  
 Db 495 EQPLPLVGSNAGVFVFWVVVVVIALVCLRKQRH-----GPDATYTEKL-QQYIAP 543  
 QY 369 RPVEFLCYSSKDGONHNVQCFAYFLQDFC-GCEVALDWDVFLSCREGRENVIOKH 427  
 Db 544 GMVYIDPTTYEDPN-EAVREFAKEIDYSCVKIEVIGAGEGECR----- 589  
 QY 428 ESOFILVCSGKMYFDKKNYKHGGGKSGKGLFLVAYSAL-----AEKLRQAKOSS 483  
 Db 590 -----GRLLKLPGRREV-VAIKTLKVGVTERRORDFLSEA 623

QY 484 AALSFIAYVEDYSCGDVPGTLDLS---TKYR-----LMDNLPQLCSHLHSDRGHQA 533  
 Db 624 SNMGQF-----DHPNIRLEGVVTKSRVMLITFEFMEHC-ALDSFLRLND----- 667  
 QY 534 EFCQIT-----RQSGRRNY-FRSKRSIYV---AIC-----NMHOFIDE 569  
 Db 668 ---GQFTVQLVGLMGRGAAGKYLSEMYVHRDLAARNILVNSLWCKVSDFGSLRFLED 725  
 QY 570 EPDWFQF-----VPEH-----PPPLRYREPVLKRFDS-----GLVLDNVCKAPGPE 612  
 Db 726 DPS---DPTYSLLGKIPINWTAPEPIAYR-----KFDASDVWISYGVHMEVNS----- 773  
 QY 613 SDPCLKVEAAVLGATGPAQSOHESQHGGLDQDGEARPAIDGSAALQPLHLTVKAGSPDM 672  
 Db 774 -----YGEQPYWNSNODDINAVEQDIYELPPHDCPTALHQLKMASCVWRNLR 822  
 QY 673 PRDSGIYD-----SSVPSSELSLPIAEGLSITDQT 701  
 Db 823 PRFSQVNTLQKLIRNAASLKVTASAPSG-MSQPLLDRTVPDIT 865

## RESULT 9

S37627 protein-tyrosine kinase (EC 2.7.1.112), receptor type - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000  
 C:Accession: S37627  
 R:Bohme, B.; Hollrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Strebhardt, K.; Ru  
 Oncogene 8, 2857-2862, 1993  
 A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.  
 A:Reference number: S37627; MUID:93390963; PMID:8397371  
 A:Accession: S37627  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <BOE>  
 A:Cross-references: EMBL:X75208; NID:G406867; PIDN:CAA53021.1; PID:G406868  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein  
 F:631-899/Domain: protein kinase homology <KIN>  
 F:639-647/Region: protein kinase ATP-binding motif  
 F:922-988/Domain: SAM homology <SAM>

Query Match 2.94; Score 115; DB 2; Length 998;  
 Best Local Similarity 19.04; Pred. No. 1.3;  
 Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 35 GADTCGRWKAARPRLC-----VANEVGVA-----SRNSG-----LYNITEK 73  
 Db 267 GACTCATGHEPAKESQCRPCPGSKAKQGEPCPCPNNSRTTSPASICTCHNNFYR 326  
 QY 74 YDN-----CTTILNPVGRHVIADAOITISQYACHQDVAVILMS-PGALGIEFLKGR 126  
 Db 327 ADSDSADSACTIVPSP-PROVISNV-----NETSLILENSEPRDLGGDDLLYN 374  
 QY 127 VILEELKSG-----RCCQILILKDPKQLNSFKRTGSESQPLLNKFFETDYFVYVPPF 181  
 Db 375 VICKKCHGAGGACSCDDNVEFVPRQLGLSEPRVHS-----HLLAHTRYTEVQAVN 429  
 QY 182 SIKNESNHPFFETTRACDILLQPDNLACKPMPKRNILNSQSGDMOVSDPHAPNFGP 241  
 Db 430 GVSGKSPPLPRYAAVNTTNOAAPSEV-----PTLRLHSSSGSLTSLNAPPERNG- 481  
 QY 242 RFFLYLKLKHEGPF-KRKTCKOBQTTTETSCLLQNVSP-GDYIIELVDDTNTTKYMHY 299  
 Db 482 --VILDYEMKY---FEKSEGIASVTTSQKNSVOLDGLOPOARYVVOV-----RARTVAGY 531  
 QY 300 A--LKPVH-----SPWAGPIRAVAITVPLVVISAFATL-----FTVMCRKQKQENIY 345  
 Db 532 GQYSRPAEFTTSERGSQAOLQLOQLPLVGSNATAGLVFVVVAVVIALVCLRKQRH----- 587  
 QY 346 HLDSESSSTVTAALPRERLRPVPKFLCYSSKDGONHNVQCFAYFLQDFC-GCEVA 404  
 Db 588 -----GSDSEYTEKL-QQYIAPGKHYIDPTTYEDPN-EAVREFAKEIDVSCVKEEV 638



QY 405 LDLMEDSLREGOREWVQIKIHESOFIIVVCSKGMKYVVDKKNYKHGGRSGKGLF 464  
 Db 639 IGAGEFGEVCR  
 QY 465 LVAVSAI-----AEKLRQKQSSAALSKFTAVYDFYCEGDPGIDLS---TKYR-----513  
 Db 662 -VAIKTAVYTERQDFLEASIMQF-----DHPNIRLEGVTKSRPVM 709  
 QY 514-----LMDNLPOLCSHLHSRDLQSPQHT-----RQSRRTY-PRSKGR 554  
 Db 710 LTFENEC-ALDSFLAND-----COFTVQLVGMKRGIAAGNKYLSEMYVHRDLAAR 762  
 QY 555 SLAY-----AIC-----NMHOFIDEEPWFKEQVFPFHP-----PLRYREP-----VLEKFD 597  
 Db 763 NILVSNLVCKVSDFGLSRLEDDPS-----DPTYSLSLAKKIPINWTAPEAIYRFT 816  
 QY 598 S-----GLVLDVNCVCKPSPESDFCLKVEAVIATGATPADSOHESQBGGLDQGEARPA 650  
 Db 817 SASDVWAGYVMVEVMS-----YGERPYWMSNQDVINAVQDYRLPPP 860  
 QY 651 LDGSAALQPLHTVYKAGSPDMPSDGIYDS-----SVPSSELSLPLMEGL 696  
 Db 861 HDCTALQLMLDCWTRDNRNLRPFSGQIVNTLDKLRNAAKLKVIASAGSGSQPLDRT 920  
 QY 697 STDQTFSSLTSSVSSSGLEGEPPALPSSKSGCKADIGCRSTYDEL 747  
 Db 921 VEDYTTTFTVGMWLDIAIK-MGRYK-----ESFVSAGFASFDVAQMTAEDL 965  
 RESULT 10  
 T17212  
 hypothetical protein DKF2p434P211.1 - human (fragments)  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17212  
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18723  
 A:Accession: T17212  
 A>Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-488;489-535 <POU>  
 A:Cross-references: EMBL:AL117401  
 A:Experimental source: Adult testis; clone DKF2p434P211  
 A:Note: the cDNA sequence contains a 1 frameshift near codon 488  
 C:Genetics:  
 A:Note: DKF2p434P211.1

Query Match 2.78; Score 110; DB 2; Length 535;  
 Best Local Similarity 23.59; Pred. No. 1.3;  
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;  
 QY 474 KLRQKQSS-SAAALSKFTAVYDFYCEGDPGCI-----LDLSTKYRLMDLQ 520  
 Db 103 RYNTQSTSWTSSCINRAISSVSTGGLPOLKRRRCPASSHCQLTLSSKTYSEDRPQ 162  
 QY 521 LCHSLHSRDLQSPQHT-----RQSRRTY-PRSKGRSLYVAICNMHOFIDEEPWFKEQF 578  
 Db 163 AVSGHTQCKEADIAPQTLT-----LRNDSSTSEASRP-----STHKF-----PLLPRRRG 210  
 QY 579 VPFH-PPPL-----RYREPVLKFDGSLVLDVNV-----CKPGPESDFCLKVEAA 622  
 Db 211 EPLMLPPLGLYRYTVEDLDREKAAFORINSALQVEDKAISSDCRPSRPSH---TLSSL 267  
 QY 623 VLGATG-PADSOHESQBGGLDQGEARPAALDGSNAALQPLHTVYKAGSPDMPS-----RD 675  
 Db 268 ATGASGLPAVRKAPS-----MDAQOETHKSDCLGLDPLASA---AGVPTAPMSGKKHRP 321  
 QY 676 SG-IYDSSVPSSELSLPLMEGLSTDQTFSSLTSSVSSSGLEGEPPALPSSKLSG 732  
 Db 322 PGLFSSSDP-----LPATSSDSQDSQAQVTSLI-----PAPFPAASMDAG 361

RESULT 11  
 I49239  
 vesicle transport protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I49239  
 R:Teillac, J.T.; McIntosh, S.; James, D.E.  
 J. Biol. Chem. 270, 5857-5863, 1995  
 A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neur  
 A:Reference number: I49238; MUID:95197608; PMID:7890715  
 A:Accession: I49239  
 A>Status: Preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-592 <RES>  
 A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PID:9642028  
 C:Genetics:  
 A:Gene: munc-18c

Query Match 2.78; Score 110; DB 2; Length 592;  
 Best Local Similarity 18.58; Pred. No. 1.5;  
 Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;  
 QY 321 LVVISAFATLFTVMCRKQ-----ENYSHLDESESSSYTAALPRELRPRR 371  
 Db 34 IMLDEFTLLSSCCMTDLLEEGITVIENTYKRRPVRQMKALYF-----ISPTK 86  
 QY 372 VFLCYSSKQDQNHMVVQCFAVLFQDF-----GCE-----402  
 Db 87 SVDCFLRDFGSKSEKKYKAAVYVTFDPCPSLKNKIKASCSSIRCKEINISFIPQESQ 146  
 QY 403 -VALDLWEDFSIC-----REGRENVIOKIHESQFIIVC-----SKGMV-----442  
 Db 147 VYILDVPDAFYCYSPDSNASRKEVVMMAEQ---IVTCATLDENPCVRYKSKPLDNA 204  
 QY 443 -----FVDRK---NYK-HKGGRSGKGLFLV-----AVSAIAEKLKQAKQSSAALS 487  
 Db 205 SKLAQLVKKLEDDYIKDEGLIKGTQSGLLIDRGDFDPVSTVLHEL-----252  
 QY 488 KFIATVFD-----YSCBG-DVPGIL-----DLSTKYR-----LMDNLPOLCSHLH 526  
 Db 253 TFGAMAYDLLPIENDTYKTDGKEAEVLEDDDLAVRVYRHRHTAVVLEIEIKLMKEIS 312  
 QY 527 SRHGLQEPQHTROGSRNYFRSKGRSLYVAICNMHOFIDEEPWFKEQFVFPHPPL 586  
 Db 313 STK-----KATGKTSLSALTQLMKKMPFRKQISKQV-----HL 348  
 QY 587 RYREPVLKFD-----DSGLVLDVNCVCKPSPESDFCLKVE 620  
 Db 349 NLAECDMKNFKLINIEKLTQDLALGDAEQVRKDSMLVLLPVL---NNHNDCKIR 406  
 QY 621 AAVLGATG-PADSOHESQBGGLDQGEARPAALDGSNAALQPLHTVYKAGSPDMPS-SCIY 679  
 Db 407 AVLLYIFGNGTTEEN-----LDRLHNKVTEDSDMKIRNWSHLG 446  
 QY 680 DSVVPSSELSLPLMEGLSTDQ 701  
 Db 447 VPVPPSQAKPLRDRSAEET 468

RESULT 12  
 T13960  
 beige protein homolog - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T13960  
 R:Morii, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.  
 submitted to the EMBL Data Library, November 1998  
 A:Description: Deletion in the beige gene of the beige rat due to recombination between  
 A:Reference number: Z17837  
 A:Accession: T13960  
 A>Status: Preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA

A:Accession: T42730  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3788 <ORF>  
A:Cross-references: EMBL:AB020019; NID:d1241953; PID:d1035670; PIDN:BA34688.1  
A:Experimental source: strain DA; spleen  
C:Genetics:  
A:Gene: beige

Query Match 2.7%; Score 108.5; DB 2; Length 3788;  
Best Local Similarity 19.4%; Pred. No. 31;  
Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;

QY 20 GSOLAAAGSGGARGADTCGRKAAARPLCVANEGVGPASRNSGLYNITFKYDNCCTT 79  
Db 651 GETAGTLCGAGSCGLPSPSYR -----QGILP-----SSGSEDLKWDALAE 695

QY 80 XLPVGVHVIADQNTISQYACH--DQAVYILMSFGGSGIEFLKFRVILEELKSG- 136  
Db 696 YQNFIPQB--DRHNTQIASHCNLIQNGNIVQW-----KLTINFPVLQGV 743

QY 137 ---ROCGLIKPKOLNSFKRTGMSQFFLANKFET-DYFVKVVP-----FP 181  
Db 744 ELVHRCOLST-----TSQTHMSQKQYLPOEVLQIYLTLPILKLSVRIDLFL 795

QY 182 SKN-----BSNT---HPE-FRTRACDILLQPNLACKPKFKPRNLINISQHSQMQ 229  
Db 796 SCGVNHLIELNLYDQIRSHLAKAFETLIVSLGEOKRAAVPGV---DGLDIQELSL 852

QY 230 VSFQAPHNFEFFVHYKLLKHEGPEKRTCKQETTTSCLLQNVSPGVILVDD 289  
Db 853 V-----GPSLHK-----QASTDSFCSLKR-----FYASLRT 880

QY 290 TWTFKYNHVALPVSHPAGIRAVAITVPLVVISAFATLFTWCKRKQENYSHLDE 349  
Db 881 DPKKKVTHQ-----DAHINTINFLCVAF-----LCVSKADSDRESAN- 920

QY 350 ESSESTY--TAALPRRLRPVKVFLCYSKDQGNHNV-----OCFAYFLQDFCGEV 403  
Db 921 ESEDTSGVDTASEPLSHMLPLSL-----ENVLPSPCLH----- 958

QY 404 ALDNEFSLCRGQREWY--IQKHESQFI-----IVCSKGMKYFVDKKNYKKGGRG 457  
Db 959 AADIW-----SMCR-----WYMLNSVFOKFLRGFGFOVCH- LIPMIQKLFPSHTEQ 1009

QY 458 SGKGELP-----LVAVSAIAEKLRQAKSSAALSKEFTAYFDYSCGQDVPCLD--- 507  
Db 1010 REQEMSVNKGALISOPMELKEDVSSSTAPEGFLKSAORVSELSQMLPTAE 1069

QY 508 ---LSTK-----YRLMDNLPQLCH---LHSRQGLQEPQHTQ 542  
Db 1070 QILATKTPGEANTFNOSEFTLQSLRLLESLLAICLHSARASQOKHELEPSQ----- 1124

QY 543 SRNFTSKSGSLYVAICNMHOFIDEEP-----DNFKQFVPPHPPPLRYEP 591  
Db 1125 -----SLSENILCELRLHLSQSKVAETELAKPLFALLRALVAGNHSADLPDGT 1174

QY 592 VLEKFDGLVNDVNCPPSPDCLKVAEAVLGATG-----PADSQHESQHGGLDQDCE 646  
Db 1175 VTKSHPS---EBVLSQPDSEAEADSQCSKLILGREGYEADSESNEDGETQDGV 1231

QY 647 ARPALDG-SAALOP--LLHTVKAG 667  
Db 1232 ELPEAEFGSGIVPNLLLESITHG 1255

RESULT 13  
T42730  
Basoon protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
R:Accession: T42730  
R:Dieck, S.; Sannarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J.; Cell Biol. 142, 499-509, 1998  
A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized  
A:Reference number: 222249; NID:98345363; PMID:9679147

A:Accession: T42730  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3942 <ORF>  
A:Cross-references: EMBL:Y17034; NID:93413809; PIDN:CAA76598.1; PID:93413810  
A:Experimental source: strain 129 SVJ  
C:Genetics:  
A:Gene: beige  
A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1  
A:Note: basoon  
C:Function:  
A:Description: may be involved in cytomatrix organization at the site of neurotransmission  
A:Note: component of the presynaptic cytoskeleton  
C:Keywords: coiled coil; zinc finger

Query Match 2.7%; Score 107.5; DB 2; Length 3942;  
Best Local Similarity 19.1%; Pred. No. 39;  
Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;

QY 516 DNLPLQCLSHLSDHGLQEPQHTROGSRNTRFKSGRSLYAIC-----NNHOFIDEE 570  
Db 3535 DTCQFCS-----SHMPDQVQEHKQDGRAHAYKREBGMDDSHCVSDSEAYHLGOEE 3589

QY 571 PDWTEKQFVPHPPVRYRE-----PVLEKE-----DSGLVLNDVNCCKPG 610  
Db 3590 TDWFDK---PRDARSDFRHHGHTVSSQKGRPARHSYHDYDEPPEGLWPHD---EGG 3643

QY 611 PESDFCLKVENAVLGNATGPNDSOHSQHG-----GLDQDG-----EAP- 649  
Db 3644 PGRH-----TSKEHRHSDHGRHSRAGEPGRRAAPHARDMGREARPH 3691

QY 650 -----ALDSALQPLHTV 664  
Db 3692 POASPAPAMOKKQGPYSSADYSQSSRAPSAHYHSAESKSGRQANTGPSALQPKADTQ 3751

QY 665 KAGSPDMPDSCGTDSSVPSSSELSPLMBGLSTDTQTSTLTSYSSSGSGEEPEPAL 724  
Db 3752 AQPMQGRQAAPGQSQPPSSROT---PSGTASRQPTQCCQCCQCCQCCQCCQCCQCCQ 3808

QY 725 PSK 727  
Db 3809 PSQ 3811

RESULT 14

T30851  
lysosomal trafficking regulator, long splice form - mouse  
N:Alternate names: beige protein homolog  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 24-Nov-1999  
C:Accession: T30851  
R:Barbosa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.  
submitted to the EMBL Data Library, September 1996  
A:Description: Two bg. or not two bg? Longest isoform of mouse Lyst (beige) gene.  
A:Reference number: 220903  
A:Accession: T30851  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3788 <BA>  
A:Cross-references: EMBL:U70015; NID:91813541; PID:91813542; PIDN:AAC53011.1  
A:Experimental source: strain C57BL/6J  
C:Genetics:  
A:Gene: Lyst  
A:Map position: 1  
C:Keywords: alternative splicing

Query Match 2.7%; Score 107; DB 2; Length 3788;  
Best Local Similarity 19.5%; Pred. No. 40;  
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;  
QY 20 GSOLAAAGSGGARGADTCGRKAAARPLCVANEGVGPASRNSGLYNITFKYDNCCTT 79  
Db 651 GETAGTLCGAGTSCGLPSPSYR-----QGILP-----SSGSEDLKWDALAE 695

QY 680 YLNPVKRVIADONITISOTACH--DOVAVTILMSPGALGIEFLKGRVILRELKSEQ- 136  
 Db 696 YQSFVQOE--DELHNIOIANHICNLLKGNVVOH-----KLYNIFNPVLRGV 743  
 QY 137 ---RQCQLIKDQQLNSFRKCHESQPLANKFET-DYFKVVP-----FR 181  
 Db 744 ELVHQCQLNSIPS-----AQTHMSQKQYLQFQEVQIYKLTPLVLLKSRVIRDLFL 795  
 QY 182 SIKN-----ESNY-----HPF-FTRACDQLLPDNLACKPFKPRNLNISQHSQMO 229  
 Db 796 SCNGVNHIELNYLDGIRSHSKAFETLIVSLGQKDAALVDV--DGLDIOQLPFLS 852  
 QY 230 VSDHAPHNFGRFFYLRYLKHESPFRRKTKQEQTTETSCILLQNSPCDYIIEILDV 289  
 Db 853 V-----GPSLHK-----QOASSDPCSURK-----FVASLRP 880  
 QY 290 TNRTRKVMHAYALKPVHSPWAGPIRAVAITVPLVVISAFATLVVMCRKQCOENIYSHLOE 349  
 Db 881 DPKKRTIH--QDVH-----INTINLELCVAF-----LCVSKADS-----DR 916  
 QY 350 ESSESSTIALPRERLRPRPVFCYCKSGQGNHNVV---OCFAIFLDPCGCEVAL 405  
 Db 917 ESANESDTGYDPPPELUSHMLPCLSLD-----VVLPSPECLH-----AA 960  
 QY 406 DLMEFSLCRGQREWV--IOTIHESQFI---IVVCSKQMYFYDKKYNKHKGGGSG 459  
 Db 961 DIN--SMCR-----WYMLNSVFOKFRILGGFQVQCHE-LIFMIIOKLFERSHTEQGR 1011  
 QY 460 KGELF-----LVAVSAIAEKLQAKQSSAALSFKFIAVTFOYSGEGVPGIL--DLSTK 511  
 Db 1012 QGEMSNENQELIRIS-----YPLTLKGVDSATAPDLGFL 1048  
 QY 512 YRLMDN-----LPOLCSHLSRHDGLQEPGQHTROGSRNRYFRSKGSRISLYAION 562  
 Db 1049 RKSADSVRGFSQPVLTSAEQIVATE--SVFGE-----RKAPNSQOSETSLQSIRL 1098  
 QY 563 MHQFIDEEDPFQKQFVPPHPPRYRPPVLEKFDLSLVINDVCK-----608  
 Db 1099 LESLID-----ICLSHARACQRMLELPSQGLSVENILCELREHLSQSKVAETE 1149  
 QY 609 -PGPESDFCLKVEAAVIGA-TGPADS-----QHSQHGGLDQGEARPAIDGSAALPLHL 662  
 Db 1149 LAKPLFDALLRVALGNHSADIGDAVTEKSHPSSEELLSQPFDESEAEQCCSLKLL 1208  
 QY 663 TVRAGSPDM---PRDSGIYDSSVPSSLSLPLMEGLSTQDTETSSLPESVSSSSGLGE- 718  
 Db 1209 GELEGYEADESNEPDVTDQGV--ELN-PEAGGFS-GSIVSNLLENLTH-----GEI 1259  
 QY 719 --EERPALPSSLSSGSKADL 738  
 Db 1360 IYPEICMLGILNLSASKALDV 1281

## RESULT 15

Db6477  
 protein F1504.27 [imported]-- Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: D86477  
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Liu, X.; Liu, Z.A.; Luo, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; PMID:21016719; PMID:11130712  
 A:Accession: D86477  
 A>Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-638 <STO>  
 A:Cross-references: GB:AE005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GN00141  
 C:Genetics  
 A:Gene: F1504.27  
 A:Map position: 1

## Query Match

2.7% Score 106.5; DB 2; Length 638;  
 Best Local Similarity 19.4%; Pred. No. 3.1;  
 Matches: 94; Conservative: 63; Mismatches: 175; Indels: 153; Gaps: 24;

QY 94 NITISQYACHDOAVTILMSPGALGIEFLKGRVILRELKSEQCOQLIKDPQLNS 153  
 Db 275 DIKQYQYCHLQDCFFVHS-----KATHENWWDGKELEWIESEDESIDSP 322  
 QY 154 FKRTMESOPFLANKFETDYFKVVPFP-----SIKNESHYPFFTRACDQLLPDNLAC 210  
 Db 323 FRLG-----DSFIKHFCHKRLKLNHDGARDTEKQCRAC---IYP--IVS 364  
 QY 211 KPMKPRNLNISORG--SDMQVSDPHAPNPGFFFLYHKLKHEGP--FKRTCKQEQT 266  
 Db 365 HQFYCKKCNVSLHEVCAGLSKLDHALN-----HTLLSPSPKKECCSACSERST 416  
 QY 267 TETTSCLLQNSPGDYIIELVDDNTTRKVMHAYALKPVHSPWAGPIRAVAITVPLVISA 326  
 Db 417 GFSYIC--SNKGCODFVLDV-----RCISLVLEYFIHRSHEH-----PIFISTS 457  
 QY 327 FATLFTVMCRKQCOENIYSHLDEESSE--SSTYTAA--LPRE---RLRPRPKVFLCYSSKDG 381  
 Db 458 YNSKDEILLCKVKCKRCGLGAHLQCTICEFTWCYSCAIIPOEIHRYFKHPLTLSCGESAD- 516  
 QY 382 QNHMVVOCFAIFLDPCGCEVALDMEFSLCRGQREWVYQIHESQFIIVVCSKGMK 441  
 Db 517 ----NTYCEV-----CEKQDPKRENYTCNK-----CCITIH-----LHCIFGSS 553  
 QY 442 YEVQKKNKHKGGGSGKGLFLVAVSAIAEKLQAKQSSAALSFKFIAVTEDYSCGD 501  
 Db 554 VFM-----KPG-----SIFDYIYGVQV 570  
 QY 502 VGIIDLSLTKVRLMDMLPOLCSHLSRHDGLQEPGQHTROGSRN--YFRSKSGSLY-V 558  
 Db 571 V-----FRNNSNTRQCYMCHNCTGL-----IFYEGYRRNATYYNNHNSRTHRM 616  
 QY 559 AICNM 563  
 Db 617 IFCSL 621

Search completed: May 6, 2003, 13:45:47

Job time: 60 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003: Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 13:34:41 ; Search time 14 Seconds  
(without alignments)  
2230.834 Million cells

Title: US-09-912-157-2  
Perfect score: 4013

Sequence: 1 MAPWLQLCSVFFTVNACLNG.....CKADLGCRSYTDELHVAAPL·753

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 segs. 41476328 residues

	Total number of hits satisfying chosen parameters	112892
0	112892	112892
1	112892	112892
2	112892	112892
3	112892	112892
4	112892	112892
5	112892	112892
6	112892	112892
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99	112892	112892
100	112892	112892

Minimum DB seq length: 0

Maximum,DB seq length: 2000000000

Post-processing: Minimum-Match 03

Listing first 45 summaries

Database : SwissProt 40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	Mismatch				
1	310	7.7		866	1	I17R_HUMAN	Q96f46 homo sapien
2	306	7.6		864	1	I17R_MOUSE	Q60943 mus musculu
3	135.5	3.4		502	1	I17S_HUMAN	Q9rm6f homo sapien
4	126.5	3.2		718	1	Y502_CAEEL	Q10128 caenorhabdi
5	115	2.9		998	1	EPB3_HUMAN	P54753 homo sapien
6	110.5	2.8		499	1	I17S_MOUSE	Q911p3 mus musculu
7	110	2.7		592	1	STB3_MOUSE	Q60770 mus musculu
8	104	2.6		1462	1	PRP6_DROME	P16620 drosophila
9	103.5	2.6		663	1	RGP2_HUMAN	P47736 homo sapien
10	102	2.5		859	1	ABR1_HUMAN	Q12979 homo sapien
11	101	2.5		1275	1	GRNP_HUMAN	Q13972 homo sapien
12	100.5	2.5		974	1	R974_HUMAN	Q43182 homo sapien
13	99.5	2.5		783	1	Z151_MOUSE	Q60821 mus musculu
14	99	2.5		794	1	ZFY2_MOUSE	P20662 mus musculu
15	99	2.5		970	1	PSU1_YEAST	P53550 saccharomyc
16	98.5	2.5		993	1	EPB3_MOUSE	P54754 homo sapien
17	98.5	2.5		1050	1	EX5B_CHLPP	Q92797 chlamydia p
18	98	2.4		820	1	CNBB_TIGR	P33223 tripeustes
19	97.5	2.4		1845	1	Z236_HUMAN	Q90i36 homo sapien
20	97	2.4		984	1	EPB1_CHICK	Q07494 gallus gall
21	97	2.4		984	1	EPB1_RAT	P07959 rattus norv
22	96.5	2.4		746	1	ABL_MLVA	P00521 abelson mur
23	96.5	2.4		902	1	EPB8_KENLA	Q91736 xenopus lae
24	96	2.4		424	1	MK09_HUMAN	P45984 homo sapien
25	96	2.4		660	1	HT31_ARATH	Q45966 arabidopsis
26	96	2.4		1114	1	E2K3_MOUSE	Q92265 mus musculu
27	95	2.4		828	1	CAN_DROME	Q11002 drosophila
28	95	2.4		933	1	PRGR_HUMAN	P06401 homo sapien
29	95	2.4		1036	1	AXO1_CHICK	P28685 gallus gall
30	94.5	2.4		351	1	HM14_CAEEL	P20271 caenorhabdi
31	94.5	2.4		770	1	G1T1_RAT	Q92772 rattus norv
32	94.5	2.4		841	1	EP63_MCMVS	Q69154 murine cyto
33	94.5	2.4		1011	1	M3K6_HUMAN	Q95382 homo sapien

## ALIGNMENTS

## RESULT 1

IL17R_HUMAN	IL17R_HUMAN	STANDARD;	PRT;	866 AA.
ID	O96F46	O43844;		
AC	15-JUN-2002	(Rel. 41, Created)		
CD	15-JUN-2002	(Rel. 41, Last sequence update)		
DDT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	15-JUN-2002	(Rel. 41, Last annotation update)		
DEFN	Interleukin-17 receptor precursor (IL-17 receptor).			
OS	IL17R.			
GN	Homo sapiens (Human).			
NCBI_TaxID	9606;			
CC	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE-T-cell;			
RC	MEDLINE-98035683; PubMed-3367539;			
RR	Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,			
RA	Mendenbos T., Zappone J., Painter S.L., Armitage R.J.;			
RT	"Molecular characterization of the human interleukin (IL)-17			
RL	receptor.";			
RF	cytokine 9:794-800(1997).			

**-1- SUBCELLULAR LOCATION:** Type I membrane protein (By similarity).

-1- TISSUE SPECIFICITY: widely expressed.

-1- PTM: Glycosylated.

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EMPR : PE9017. 33000730

EMBL: U38917; AACB99730  
EMBL: BC011624; AAC11624

Genew; HGNC:5985; IL17N

MIM; 605461; - .

Receptor; Transmembrane	1	31
SIGNAL		

CHAIN	32	866
CHAINED	1	51

DOMAIN	32	320
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TRANSMEM	321	341
DOMB IV	342	956

DOMAIN:	342	898
DOMAIN	810	818

CARBOHYD	49	49
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CARBOHYD	54	54
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CARBOHYD<sup>2</sup> 206

FT CARBOHYD 225 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 242 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 265 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CONFLICT 367 V -> A (IN REF. 1)  
 FT CONFLICT 580 H -> R (IN REF. 1)  
 SQ SEQUENCE 866 AA; 96131 MW; 28330BED2303B0C9 CRC64;

Query Match 7.7%; Score 310; DB 1; Length 866;  
 Best Local Similarity 23.1%; Pred. No. 5.4e-16;  
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

Qy 69 NITFYKNC--TTLNPNVGRHVIADQNT-----ISOYACHDQ-----VAVTILMS 113  
 Db 49 NCTVNSCLDSDSHIP-----RNLTPSPFKDLQDQHFHFAHQDGLFVAHIEMT 99  
 Qy 114 -PCALGIEFLGFRVILELSEGRQCOQLIKDPKQLNSFKRTGMSOPFLNMKFED 172  
 Db 100 LOTDASILYLEGALSVLQNTNRLVR--FEFLSKLHRRHWRFTFSHFV-VDPOE 156  
 Qy 173 YFVKV--VPFPIKSNSTHPPFFTRACDILQDNLACK---PFWKPNL----- 219  
 Db 157 YETVHLLPDPDQPNQSNFLVPCDHAKMKTTPCMSSGSLMDP-NITVETLEAH 215  
 Qy 220 -----NISQSGDMQVSDHAPHNFGFRFFYLHYKLKHBOPKRTKCOEOTETT 270  
 Db 216 QURVFTLWNESTHYOILTSPPHENISCFEIMH-HIPAPPEEFHORSNVTLRLNK 274  
 Qy 271 SCILQNVSPGDYIIELVDDT-----NTRKVMHYALKPVHSPNAGPIRAVAITVPLVVISAF 327  
 Db 275 GCRCRQVQIOFPSSCLNDCLHSAVTSCPEMDTPERTPYDMLVYWEITGISTLLVG 334  
 Qy 328 ATLFTVCKRQKQENIYSHLDRESESESTYTAALPRERLRPP---KVLCTSSKDGON 383  
 Db 335 SVILLIVCKWRLAGPS---BKYSDDTKYDGLPVADLIPPLKPKRWIISA-DHPL 390  
 Qy 384 HANVVOCAFVLODFCGCEVALDWEDFSILCREQEWY----TOKIHESOFILVCSKG 439  
 Db 391 YDVVVLFAEQFLTACGTEVALDLEBOALSEAGVNTWGRQKQENYKSLIVLCRSG 450  
 Qy 440 MYFVDKNTYKHGG-----RSGKGEFLVAVSAIAKLRQAKQSSAALSKEFIA 491  
 Db 451 TR-----AKWALLGRGAPVRLRCHDGRPVGLDFTAAANNILPDFKR-----PACFGTVV 501  
 Qy 492 VTF-DYSCGDPGVLIDLSKYKVMNLPCLSHLSRDHGLQEPQHTROG--SRRNYF 548  
 Db 502 CYFSEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIQDLENFQGRMHRVGLSGDNYL 559  
 Qy 549 RSKGRSLTVAICNMHQFIDEPWFE-----KQVPPHPPPLRYRPPVLEKFDGSL 600  
 Db 560 RSPGCRQLAALDRFDMOVHCPDWFECENLYSADQDAPSLDEEV-FEPLLP-GTGI 617  
 Qy 601 VLNDVCKPQPSDFCLKVEAAVLGANGPADSOHE-----SOHGG 640  
 Db 618 VKRAPLYRE-PGQACLAIDPLVGEEGAVALKLEHLPQPGQAPAPOLHTLVLAEEGA 676  
 Qy 641 LDQDEARPALDGA---ALO-----PLHTVKAQSPMDRSGIYDSSVPSSELSLP 691  
 Db 677 LVNAVEGPLADGAANVRLAAGEACPLGSPGAG-----RNSVLF--LPVDPEDSP 727  
 Qy 692 IAMEGLSTDOTETSLTESVSSSGLEEPPALPSKLLSSGSKADLGC 740  
 Db 728 L--GSSTPMASPOLLPEDVR-----EHLGLMLSLFQSLSLSCQAQGC 768

## RESULT 2

IL17R\_MOUSE  
 ID IL17R\_MOUSE STANDARD; PRT; 864 AA.  
 AC Q60943;  
 DT 15-JUN-2002 (Rel. 41; Created)  
 DT 15-JUN-2002 (Rel. 41; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor)  
 GN IL17R.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OCI Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 NC TISSUE=Thymic lymphoma;  
 RX MEDLINE=96111968; PubMed=8777726;  
 RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,  
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;  
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 RT novel cytokine receptor.";  
 RL Immunity 3:811-821(1995).  
 CC -1-FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
 CC suggesting that additional components are involved in IL17-induced  
 CC signalling (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC  
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 CC  
 CC EMBL; U31993; AAC52357.1;  
 DR MGD; MGI:107399; IL17r.  
 KW Receptor; Transmembrane; Signal; Glycoprotein.  
 FT SIGNAL 1 31 POTENTIAL.  
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.  
 FT DOMAIN 32 322 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 323 343 POTENTIAL.  
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 809 814 POLY-GLU.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 7.6%; Score 306; DB 1; Length 864;  
 Best Local Similarity 22.5%; Pred. No. 1.1e-15;  
 Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

Qy 40 GWRM-----KAARPEL-----CVANEGVGPASRNSGLYNTKYDNCYTLNPGK 86  
 Db 17 GWLLLLNLVAFGRASPLLPDFPAPVCAQEGISCRVNSTCLDDSWHFNKUTFSSPKNI 76  
 Qy 87 HVIADAQNTISYACHQOAVT-ILWS-PGALGTEFLKGRVILSELKSEGRQCOQ-----141  
 Db 77 YI-----NLSVSTQRGELVPLVHVTLOTDSILYLEGAELSVLQNLNRLCVKPFQ 131  
 Qy 142 -LILKDPKQLNSFKRTGMSOPFLNMKFEDYEVVYVFPFSPKSNESYHFFFTTRAC 199  
 Db 132 LSLMLQHRKRWRFSE-----SHFVDPQGEVTVVHLKPPIPDGDPNHRKSIIFVDC 185  
 Qy 200 D---LILQDNLACKPFKPNRLNI---SOH-----GSDMQV 230  
 Db 186 EDSEKMKNTTSCVSSGSLMDP-NITVETLOTQHLRVDFTLNNESTPQVILLESFSDSENHS 244  
 Qy 231 SFD-----HAPHNFGFRFFLYNKLKHE---GPFKRTCKOEQTETTSCLL 274  
 Db 245 CFVVVKOIFAPQEEFHORANVTTLSKFHCCHHHVQVQPF-FSSCLND-----CLR 296  
 Qy 275 QNVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-NA-GPIRAVAITVPLVVISAFATL 330  
 Db 297 HAVTVPCPVI-----SNTT-----VPRKPADYIPLAWYIGLITLAI-----LLVGSVIL 341  
 Qy 331 FTVNCRKQKQENIYSHLDRESESESTYTAALPRERLRPRKRVFLCTSSKDGONNMNVQC 390

Db 342 ICHTWLISGDOERKDDSKINGILPVLADITPPPLPR-KHIVISA-DHPLTVEVLK 399  
 QY 391 FATPLADFCGCGVALDWDGFSICREGREWYOK-----IHESQIIVVCSKGMKYPVK 446  
 Db 400 FAQLITAGCTEVALDLEQVISEYGVMTVSRQKQWENSKIIILCSRG-----TQ 454  
 QY 447 RYKAKHGG-----GRSGKGEFLVAISAIEKLRQKQSSAALSFKTAVFDY 496  
 Db 455 AKWKALIGWAEPAVLQRCDHWKDPAGDLFTAMNMLPDRF-----PACFGTYVVCVFS 509  
 QY 497 SC-EGDVGILDLSTKYLMDNLPLCGLHLSRDHGLQEPGQ--HTRGSRNFRSKSG 553  
 Db 510 ICSERDVPDLNLSRYPLMDREEV--YFIQDLNFEESRMHVRLETGDNVLOSPG 567  
 QY 554 RSLVAICMGHOFIDEPDFEKFQVPPHP-----PPLR--YREPVLKFGSGLYLVDM 606  
 Db 568 KQKRAVLAFQWOTQCPDWFRENICLADQDPLSLDEVFEDPLPP-CGGYVKKOPL 626  
 QY 607 CKGPESDCLKVAEVLGANGPADSGHESGGILDQ-----GEAR 648  
 Db 627 VRELPSDGLVYDVCV-----SEESRAKLDPQLPQRELVAHTLQSMVLPABQV 677  
 QY 649 PALDGAALQPLHTVYKAGSPDMP--RDS-----GYDSSV--PSSELSLEL----- 692  
 Db 678 PA--AHVVEPLHLPDGSAAALPMTEDSEACPLLGQVQNSILCLPVDSDLLCLCSTPM 734  
 QY 693 -----MEGLSTDOTETSLTESVSSSGLEGEPPALPSKLLSGSCRADLGCSTYDE 746  
 Db 735 MSPDHQDAREDSLEMLSLVLOSLSGOPLESWPR-PEVLE-----GCTPSEE-784

RESULT 3  
 IL17S-HUMAN STANDARD; PRT: 502 AA.  
 ID Q9NRM6; Q9NR62; Q9NR64; Q9NR65;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1), (IL-17R1), (IL17R1) (Cytokine receptor CRL4).  
 GN IL17BR-OR-EVI27.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE-2073723; PubMed-10815801.  
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shaginmasy J.D. Jr.,  
 FT "Evi27" encodes a novel membrane protein with homology to the IL17 receptor.  
 RL Oncogene 19:2098-2109(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Lung;  
 RX MEDLINE-20317118; PubMed-10749887;  
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J., Barber M.C., Wang W., Wachen K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A., Carrell J.A., Ebner R.;  
 RA "A novel cytokine receptor-ligand pair: Identification, molecular characterization, and in vivo immunomodulatory activity".  
 RT J. Biol. Chem. 275:19167-19176(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Zhang W., Cao X.;  
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Cervix;  
 RA Strausberg R.;

Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RL FUNCTION.  
 RN PubMed-11058597;  
 RP Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;  
 RA "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17R1".  
 RT J. Biol. Chem. 276:1660-1664(2001).  
 RL  
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here), and 2; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly in fetal and adult liver, kidney, pancreas, testis, colon, brain and small intestine; not detected in peripheral blood leukocytes, lymphoid organs, and most cell lines.  
 CC  
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 CC  
 CC EMBL: AF208110; AAF86051.1;  
 CC EMBL: AF208111; AAF86052.1;  
 CC EMBL: AF212365; AAF87876.1;  
 CC EMBL: AF250309; AAH37428.1;  
 CC EMBL: BC000980; AAH00980.1;  
 CC Genes: HGNC:18015; IL17BR.  
 CC MIM: 605458;  
 CC Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 KW SIGNAL  
 FT CHAIN 1 17  
 FT DOMAIN 18 502 INTERLEUKIN-17B RECEPTOR.  
 FT TRANSMEM 18 292 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 293 313 POTENTIAL.  
 FT DOMAIN 314 502 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 283 283 LTPVPTGSDICIRHGTWVLCPTGVPFPLDNKSKPG  
 FT VARSPLIC 250 288 -> VKFSELLGKGGHRLPHSLLSNLSALLPADT  
 FT S (IN ISOFORM 2).  
 FT VARSPLIC 289 502 MISSING (IN ISOFORM 2).  
 FT CONFLICT 6 6 L -> I (IN REF. 1).  
 FT CONFLICT 422 426 LFPLA -> SSPCL (IN REF. 2).  
 FT CONFLICT 427 502 MISSING (IN REF. 2).  
 FT CONFLICT 468 468 L -> F (IN REF. 1).  
 SQ SEQUENCE 502 AA; 55884 MW; CDB87586FAAE49CC CRC64;  
 Query Match 3.4%; Score 135.5; DB 1; Length 502;  
 Best Local Similarity 20.1%; Pred. No. 0.0078;  
 Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;  
 QY 218 NLMSHQSDQVQSF-----DHAPHNGFRFFLVKLAHEGPPFRKTC----- 261  
 Db 143 NANNEDGFSMSVNFPTPGCLDI-----IMKYN-----KCKVAGSLWDPN 183  
 QY 262 -----KQEQTE---TTSCLLQNVSPGYIELVDVNTTRKVMHVALKPVHSPWAGPIR 313  
 Db 184 ITACKNEETVEVNFPTPL-----GNRYMALIQMSTI-----IGFSQVFEPRKQKT 231  
 QY 314 AVAITVPLVVISAFATL-----FTVMCRKKQEQENIYSHLDESESS 355  
 Db 232 RASVIVPTVGDSEGATVQLTPPTPGSDCIRHGTWVLC-----PQGVFPFLDNKSKPG 288

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QY 356 TYTAAI-----PRKFLVYSSKDGQNMN 386
DB 289 GWLPLLLSLVATWLVAGIYLAWRHERIKKTSFTSTLTLPKLVLYPSEICFHH-- 346
QY 387 VVQCFAYFLDCCGCGVALDWDGSLCRGQRENVIOKHESOFILVCSGKMGFYVDK 446
DB 347 RICFTFLQHCGRSEVLEKQKKIENGFPWMLAKKADKVVLLSDNVSVDG 406
QY 447 KNYKGGGSGKGLFLVAVSAIAEKLRQAKSSAALSKFIAYFYDSCGDPVGL 506
DB 407 TCGSESGSPNSO-DLFLAPNLFCSDLR-----SQTHLEKTVVYFREDTKDDYNAL 460
QY 507 DLSTKRLMDNLPOLCSHL 525
DB 461 SVCPKYLHMDATAFCAEL 479

RESULT 4
ID YS02 CAEL STANDARD; PRT; 718 AA.
AC Q10128;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 81.6 kDa protein F56D1.2, in chromosome II precursor.
GN Caeenorhabditis-elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caeenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Chisoe S., Wilson R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC or send an email to licenses@isb-sib.ch)
CC
CC EMBL; 039997; AAA81100.1;
CC WormPep; F56D1.2; CE01970.
CC Hypothetical protein; Transmembrane; Signal.
KW SIGNAL
FT CHAIN 1 30 POTENTIAL.
FT TRANSMEM 31 718 HYPOTHETICAL PROTEIN F56D1.2.
FT TRANSMEM 373 393 POTENTIAL.
SQ SEQUENCE 718 AA: 42B9E056288417AA CRC64;

Query Match.
Best Local Similarity 3.28; Score 126.5; DB 1; Length 718;
Matches 82; Conservativity 21.18; Pred. No. 0.064; Indels 94; Gaps 19;

QY 363 RERLRPRP-----KVLVYSSKDGQNMNVQCFAYFLDCCGCEVALDWDGFS 412
DB 398 RDKVRSREVRNTALTFFVKVMIVAD-DNDLHTDCVKKLVLENLNCASCDPVFLEKLIT 456
QY 413 LCRGQRENVIOKHESOFILVCSGKMGFYVDKKNYKGGGSGKGLFLVAVSAIA 472
DB 457 AEQIVPSRLVQDQISSLKKFLIVVSDCAEKILDTEASTHQLVQARFPADLFGPAMEMI- 515
QY 473 EKLQAKQSSAALSKFIAYFYDSCGDPV---GILDSTKRLMDNLPOLCSHLSDR- 529
DB 516 --INDATHNEPEARKYAVRENY--PHVPPNLAIALNLT-PILPEQAQUTAFLANVE 570
QY 530 HGLQEPQCHTQGRSRRNFRSKGRSLY---VAICNMHQFIDEEDPWFKEQFVP- 580
DB 571 H-----TERANVTQISAQIHEWNLCSRMHMSFFVRPNPNLETRMKPKDLAA 619

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QY 581 FHPPLRYREPVLKFDLSGLVNDVNMCKPGPESDFCKLVAANVLGATGPDQSQHSQHG 640
DB 620 LR-----LERSPVIVIQP-----BED-----RIASIKYKLYPPQALVDS- 657
QY 641 LDQGGPAPALDGSAAQLPFLFTVVKAGSPDM--PRSGIYDSSVSPSSLSLPLMEGLST 698
DB 658 -DED-----DVDLQDP--HASHONQPLILLPPECG-----PDSD-----SD 690
QY 699 DQETSLSLTVSSSSGIGSEEPALPSK 727
DB 691 SEDSSSESESDNEG---EDPKTIIVK 716

RESULT 5
ID EPB3 HUMAN STANDARD; PRT; 998 AA.
AC P54753;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-B receptor.3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor HEK-2).
GN EPB3 OR ETK2 OR HEK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RX MEDLINE=93390963; PubMed=8397371;
RA Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,
RA Streibhardt K., Ruebsamen-Waigmann H.;
RT "PCR mediated detection of a new human receptor-tyrosine-kinase, HEK
RT 2."
RL Oncogene 8:2857-2862(1993).
CC
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
CC EPHRIN-B1 AND -B2.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: UBICUITOUS.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC
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CC
CC EMBL; X75208; CAA53021.1;
CC HSP; P29323; IBAF.
CC Genew; HGNC:3394; EPB3.
CC MIM; 601839;
CC InterPro; IPR001090; Ephrin_receptor.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003962; FNIII_repeat.
CC InterPro; IPR001660; SAM.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR001426; YKase_receptorv.
CC Pfam; PF000411; fn3; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00536; SAM; 1.
CC Pfam; PF01404; EPH_lbd; 1.
CC PRINTS; PRO0014; FNTYPEIII.
CC PRINTS; PRO0109; TYRKINASE.
CC ProDom; PD000001; Euk_pkinase; 1.

```



QY	514	---	LMNIPQLCSHLMSRHHGLQEPQGH	-----	ROGRRRY-PRSKSGR	554	
DB	710	LT	FEHNC-ALDSFLRND	---	QGFVIQVGLMGLRTAAGMKYLSBNVYHRLDAAR	762	
QY	555	SLVY	---AIC	---NHQFIDDEEDFKQFVPHPP	---	PLVREP---VLEKFD	597
DB	763	NILVNSNLVCKVSQDFGLSRFLDDPS	-----	DPTITSSLGGKIPTRMTAPEATAYKFT	816		
QY	598	S	---	GLVLMNDVCKRGPESQCLKVEAAVLGATGADPSQHSQSGGLDQGEARPA	650		
DB	817	SASDVHSGYIVMEVAS	-----	YGERPYDMNSQDVINAVEQDYRLPPP	860		
QY	651	LDGSAALQPLHETVKAGSPDMRDSGYDS	-----	SVPSSELSLPLWELG	696		
DB	861	MDCPALHQLMLDCWVRDRNLRPKFSQIVNTLKLIRNAASLKVIAASQSGSQPLDRT	920				
QY	697	STQIETSSLTSEVSSSGIGEEPPALPSKILLSGCSKADLCRSYFDEL	747				
DB	921	VPOITTFITGVMDLAIK-NGRYK	-----	ESPVSAGFASFDLVQAQMTAEDL	965		
	RESULT 6						
	IL17S.MOUSE						
AC	ID	IL17S.MOUSE	STANDARD;	PRT;	499 AA.		
AD	Q9UIE3;	Q9UIP2;					
DT	15-JUN-2002	(Rel. 41, Created)					
DT	15-JUN-2002	(Rel. 41, Last sequence update)					
DT	15-JUN-2002	(Rel. 41, Last annotation update)					
DE	Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17Rhl) (IL17Rhl) (IL-17ER).						
DE	IL178R or EVI27						
GN	Mus musculus (Mouse).						
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.						
OC	NCBI_Taxid=10090;						
ON	[1]						
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2):						
RP	MEDLINE-2073223; PubMed-10815801;						
RX	Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shaughnessy J.D. Jr.						
RA	"EVI27 encodes a novel membrane protein with homology to the IL17 receptor."						
RT	OncoGene 19:2098-2109(2000).						
RL	FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.						
CC	1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).						
CC	2- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.						
CC	3- TISSUE-SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid cell lines.						
CC	4- MISCELLANEOUS: EVI27 is a common site of retroviral integration in BXH2 murine myeloid leukemias, localized near the IL178R gene. Proviral integrations result in increased expression of IL178R on the cell surface.						
CC	5- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/announcement/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).						
CC	EMBL; AF208108; AAF86049.1;						
DR	EMBL; AF208109; AAF86050.1;						
DR	MGI; 1355292; IL17br.						
KW	Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.						
FT	SIGNAL	1					
FT	CHAIN	18	499				
FT							

FT DOMAIN 18 286 EXTRACELLULAR (POTENTIAL)  
 FT TRANSNEM 287 307 POTENTIAL  
 FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL)  
 FT CARBOHYD 67 67 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 103 103 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 156 156 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 197 197 N-LINKED (GLNAC) (POTENTIAL)  
 FT VARSPLIC 103 216 LHMVTKKCTKCTGSLMDPDITCKKKNKGVNFTNPL  
 FT FT GNRVTLLIQDFTLG -> TRENTVEVSGVFAAKHQALRI  
 FT FT SAPFLQPPGSDSVLLPPOPLASLFDHFVKLT (IN  
 FT FT ISOFORM 2)  
 FT VARSPLIC 219 499 MISSING (IN ISOFORM 2)  
 FT SEQUENCE 499 AA; 55617 MW; C66440430E3C31F3 CRC64;  
 Query Match 2.8%; Score 110.5; DB 1; Length 499;  
 Best Local Similarity 24.1%; Pred. No. 0.66;  
 Matches 40; Conservative 27; Mismatches 82; Indels 17; Gaps 4;  
 QY 355 STYTAALPRRLPRPVKXSSKDGONHNVQCFAYFLQDFGCEVALDWFSLC 414  
 DB 314 STKSPSTMLLPLKLVVYVPSICFHR--TVCRFDLONICESEVILKWKKTA 371  
 QY 415 REGOREWVIOKIHESQILIVVCSKGMKVFVDKKNYKKGGRSGKGEFLVAVSAIAEK 474  
 DB 372 EMPGVHLLTQKQADKVPFLPSVPLCDSCAGHREGSARENSQ-DLEPLAFNFCSD 430  
 QY 475 LRQAKSSAALSFIANYFDYSCEDVPGILDSTKYRMNLQO 520  
 DB 431 F-----SSQTHLYLVVYL-----GGADLKGDYNAISVCPQ 462  
 RESULT 7  
 STB3\_MOUSE STANDARD; PRT; 592 AA.  
 AC Q60770;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Synxatin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3).  
 GN STXBP3 OR UNC18C.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95197608; PubMed=7890715;  
 RA Tellam J.T., McIntosh S., James D.E.;  
 RT "Molecular identification of two novel Munc-18 isoforms expressed in  
 RL non-neuronal tissues.";  
 RL J. Biol. Chem. 270:5857-5863(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE=Brain;  
 RX MEDLINE=96421662; PubMed=8824310;  
 RA Gengyo-Ando K., Kitayama H., Mukaida M., Ikawa Y.;  
 RT "A murine neural-specific homolog corrects cholinergic defects in  
 RL Gaenorhabdittis elegans unc-18 mutants.";  
 RL J. Neurosci. 16:6835-6702(1996).  
 CC -1- TISSUE SPECIFICITY: OBITUOUSLY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE STXBP/UNC-18/SECI FAMILY.  
 CC  
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 CC  
 CC EMBL; U19521; AAA69913.1;  
 CC EMBL; D50758; BAA19476.1;  
 CC MGD; MGI:107362; Stxbp3.

DR InterPro: IPR001619; Sec1-like.  
 KW Pfam: PF00995; Sec1; 1.  
 KW Protein transport; 67942 MW; 787497IDE107871A CRC64;  
 SQ SEQUENCE 592 AA; 67942 MW; 787497IDE107871A CRC64;  
 Query Match 2.7%; Score 110; DB 1; Length 592;  
 Best Local Similarity 18.5%; Pred. No. 0.92;  
 Matches 93; Conservative 64; Mismatches 157; Indels 186; Gaps 22;  
 QY 321 LVVISAFAATLFTVNCRRKQO-----ENIYSHLDESSSTYTAALPRRLPRK 371  
 DB 34 IMLEDEFTKLLSCCKMTDLLEGITVIENIYKREPVRQKALYF-----ISPTPK 86  
 QY 372 VFICYSSKDGONHNVQCFAYFLQDFC-----GCE-----402  
 DB 87 SYDCELRDFGSKSEKKYKAAIYFDFCPDPSLKNKIKASCSIRCKEINISFIPQESQ 146  
 QY 403 VALDLWEDFSLC-----REGOREWVIOKIHESQILIVVCSKGMKVFVDKKNYKKGGRSGKGEFLVAVSAIAEK 442  
 DB 147 VYLDVDPAFYCYSPDPSNASKKVVWEMAEQ--IVYVCATLDENPGVYKSKPLDNA 204  
 QY 443 -----FVDRK--NYK--HKGGRSGKGEFLV-----AVSAIAEKLRQAKSSAALS 487  
 DB 205 SKLAQLVEKKLEDTYKIDENGLIKGTOSQLLIIDRGFPVSTVLHEL-----252  
 QY 488 RFIAYVFD-----YSCBG-DVPGIL-----DLSTKYR-----LMONLPLQCSHLH 526  
 DB 253 TFQAMAYDPLPIENDTYKYTKDGEKAEVLEDDDLWVRHRHIAVYVLEIPKLAKETS 312  
 QY 527 SRDHGLQPGQHTQGRSRRNYRSKGSYLVAVICNNHQFIDEEPDMFEKQFVFPHPPL 586  
 DB 313 STK-----KATEGRTSLSATLTOLMKKPHPRKQISKQV-----HL 348  
 QY 587 RYREPVLEKF-----DSGLVNDVNCCKPESDDECLKVE 620  
 DB 349 NLAEDCKMKFKLNEKLECKTEODLALGTADGQVRKDSMLVLLPVL--NKNEDNCKIR 406  
 QY 621 AAVLGATGPDASQHSQHGGLDQDGEARPALDSSAALQPLHTYKAGSPDMDRD-SGII 679  
 DB 407 AVLLIFINGNTTEEN-----LDRLHNKIEDSDSCHIRNWSHLG 446  
 QY 680 DSSVPSSELSLPLMEGLSTQDT 701  
 DB 447 VPIVPSQQAQKPLKDRSAET 468

RESULT 8  
 PTP6\_DROME STANDARD; PRT; 1462 AA.  
 AC P16620;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase DTPP precursor (EC 3.1.3.48) (Protein-  
 DE tyrosine-phosphate phosphohydrolase).  
 GN PTP69D OR DTPP.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Struelli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 RT and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT DTPP IS A CELL ADHESION RECEPTOR.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
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EMBL: M27699; AAA28842.1;  
 PIR: B36182; B36182.  
 HSP: P18052; LYFO.  
 FlyBase: FBan0014007; Ptp69D.  
 InterPro: IPR003961; FN\_III.  
 InterPro: IPR003006; IG\_WC.  
 InterPro: IPR003598; IG\_C1.  
 InterPro: IPR003600; IG\_Like.  
 InterPro: IPR003677; TYR\_phosphatase.  
 InterPro: IPR000442; TYR\_PP.  
 Pfam: PF00041; fn3; 3.  
 Pfam: PF00047; Ig; 2.  
 PRINTS: PR00102; Y\_phosphatase; 2.  
 PRINTS: PR00700; PTPPHPTASE.  
 SMART: SM00060; FN3; 3.  
 SMART: SM00410; IG\_Like; 1.  
 SMART: SM00408; IGC2; 1.  
 SMART: SM00194; PTPC; 2.  
 PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 PROSITE: PS00383; TYR\_PHOSPHATASE\_2; 2.  
 PROSITE: PS00056; TYR\_PHOSPHATASE\_PTP; 2.  
 Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 Cell adhesion; Immunoglobulin domain; Repeat.  
 SIGNAL  
 1 23  
 FT CHAIN 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP.  
 FT DOMAIN 24 805 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 806 823 POTENTIAL.  
 FT DOMAIN 824 1462 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 38 119 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 147 221 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 332 437 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 438 538 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 1208 1459 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 1097 1097 BY SIMILARITY.  
 FT ACT\_SITE 1391 1391 BY SIMILARITY.  
 FT DISULFID 154 214 POTENTIAL.  
 FT DISULFID 154 214 POTENTIAL.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 58 58 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 64 64 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 429 429 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 451 451 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 516 516 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 701 701 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 755 755 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 1462 AA; 167411 MW; F8091D69E88230EB CRC64.

Query Match

2.6%; Score 104; DB 1; Length 1462;

Best Local Similarity 20.08; Pred. No. 9.4;  
 Matches 88; Conservative 53; Mismatches 136; Indels 164; Gaps 23;  
 QY 55 NEGUGPASR-----NSGLNNTFKVD-----NCTYLNPGVGHVADA 92  
 DB 259 NDNDRPQKFFITQEAETPTFYHDFNGSHSYILDHFKNTTYFIRIVKNSING 318  
 QY 93 -----QNTISQYACHDOV-----AVTILWSPGALG-IIEFKGFVILEEL 132  
 DB 319 OPTQYQGGITLSY---DPFIPKVTGTSTASTITIGWPPPPDLIDYIYELIYSE- 374  
 QY 133 KSEGROCOOLILKDPKOLNSESFKTKMESQPLNKKPETYFKVVPFSPKNSNTHPF 192  
 DB 375 --SG-----EVEKVEEAIQQNSRLPYM-----FDKLTATDYE-- 408  
 QY 193 FFRTRACDILLOPDNMLACKPPY-----KRNINLSOH-----GSDMOVSP 232  
 DB 409 -FRVRACSLTIT---TCGP-NSENVNGTMDGVATPFLNLSQCHDNVTRGSIINW 462  
 QY 233 DHAPHNFGFRFPYL-----HYKLKHE--GPKKRTC--- 261  
 DB 463 DVPKTPNGKVVSYLIHLGNPMSTVDREMMGPKIRRIDEPHHTLVESVSPNTYTVS 522  
 QY 262 ----KQEQTTTETTSCLQNVSPQDIIELVDDTNTTRKVMHYALK---PVHSPWAGPIR 313  
 DB 523 AITRHKNGEPATGSLAPVSTPDATGRMWSKVNLSK---VVLKLYLPKRISERNGP1- 578  
 QY 314 AVAITVPLVVISAFATLFTVMCRKQOE-----NIYSHLDEES---SESSTYTAALPR 363  
 DB 579 -----CCRYLYLVRLNNDKELPOPEKLTATQEVHSDNVTSSYIAEMIS 626  
 QY 364 ERLPRPKVFLCYSKQGNH 384  
 DB 627 SKYF-RPEIFLGAERFSENN 646

## RESULT 9

RGF2\_HUMAN  
 ID RGF2\_HUMAN STANDARD; PRT; 663 AA.  
 AC P47736;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rapi1 GTPase activating protein 1 (Rapi1GAP).  
 GN Rapi1GAP  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RX MEDLINE=91256304; PubMed=1904317;  
 RA Rubinfield B., Munemitsu S., Clark R., Conroy L., Watt K.,  
 RA Crosier W.J., McCormick F., Polakis P.;  
 RT "Molecular cloning of a GTPase activating protein specific for the  
 RT Krev-1 protein p21rasl.";  
 RL Cell 65:1033-1042(1991).  
 [2]  
 RN TISSUE SPECIFICITY, AND INDUCTION.  
 RP MEDLINE=98010656; PubMed=9346962;  
 RA Kurachi H., Wada Y., Tsukamoto N., Maeda M., Kubota H., Hattori M.,  
 RA Iwai K., Minato N.;  
 RT "Human SPA-1 product selectively expressed in lymphoid tissues is a  
 RT specific GTPase-activating protein for Rapi and Rapi2.";  
 RL J. Biol. Chem. 272:28081-28088(1997).  
 CC -1- FUNCTION: GTPase activator for the nuclear ras-related regulatory  
 CC protein RAP-1A (KREV-1), converting it to the putatively inactive  
 CC GDP-bound state.  
 CC -1- SUBCELLULAR LOCATION: Associated with Golgi membranes.  
 CC -1- TISSUE SPECIFICITY: Significant expression seen in the brain,  
 CC kidney and pancreas. Abundant in the cerebral cortex and expressed  
 CC at much lower levels in the spinal cord. Not detected in the



Interfero, IFR0000179, RHO GAP.  
 P1am, PF001186, C2, 1.  
 P1am, PF001186, PH, 1.  
 P1am, PF006210, RHO GAP, 1.  
 P1am, PF006210, RHO GAP, 1.  
 SMART, SM002239, C2, 1.  
 SMART, SM002239, PH, 1.  
 SMART, SM002233, PH, 1.  
 SMART, SM003244, RHO GAP, 1.  
 SMART, SM003245, RHO GAP, 1.  
 PROSITE, PS500004, C2\_DOMAIN, 2, 1.  
 PROSITE, PS500010, DB, 2, 1.  
 PROSITE, PS007411, DB, 1, 1.  
 PROSITE, PS500003, PH\_DOMAIN, 1.  
 Guanine nucleotide releasing  
 DOMAIN, 91, 284  
 DOMAIN, 301, 459  
 DOMAIN, 463, 595  
 DOMAIN, 561, 805  
 DOMAIN, 417, 420  
 VARSPLIC, 1, 82

factor; Alternative splicing.

MEPSLRHGPRLSWIDTLYSNFSYCTDEYDGEHQKQPP  
 EGSETMPTIDSPSTNQSLSAQSGDGVGPTTPPEGLAP  
 -> MEEEEEAIGLDKLVLEDVFLLEECELTGTPSPGSGS  
 PFVLAVK (IN SHORT ISOFORM)  
 R -> G (IN REF. 2).  
 RSKV -> VQGA (IN REF. 2).  
 L -> V (IN REF. 2).  
 9FD50CD54FA99483 CR:64;

Query Match 2.5%; Score 102; DB 1; Length 859;  
 Best Local Similarity 20.5%; Pred. No. 6.4;  
 Matches 117; Conservative 57; Mismatches 190; Indels 208; Gaps

116 ALGIEFLAGPR---VILBEAKSGROOOL---ILKDKPQLNSSFRTGNESQPLNN-K 168  
 80 AFGVAGKGLDMKRLVLSGFLASREIYNOLKALLPKMPT---RATATTSOPVLATCO 135

[illegible]







DB 207 AAZAALSSSEBQNEVPASKG--EDQEEBAGPATVKEGKH--LNGEPEENESA 263  
QY 678 IYDVSPPSELSIP---LMEGLSTDDTETSSLTSSVSSSGLEE 719  
DB 264 GTDS---GOELGNEQNLRSQTYGDRTESKAYGSIHKCEDCGRE 305

RESULT 14  
ZFY2\_MOUSE  
ID ZFY2\_MOUSE STANDARD: PRT: 783 AA.  
AC P20662;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zinc finger Y-chromosomal protein 2.  
GN ZFY2 OR ZFY-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99158416; PubMed=2493989;  
RA Mardion D.C.; Page D.C.;  
RT "The sex-determining region of the mouse Y chromosome encodes a protein with a highly acidic domain and 13 zinc fingers.";  
RL Cell 56:765-770(1989).  
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC FINGER PROTEINS. ZFY/ZFY SUBFAMILY.

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DR EMBL; M24401; AA56845.1;  
DR FIR; A34391; A31491.  
DR HSP; P08048; 52NP.  
DR MGD; MG1:99213; Zfy2.  
DR InterPro; IPR000822; Znf\_C2H2.  
DR Pfam; PF00096; zf\_C2H2; 13.  
DR PRINTS; P000048; ZINCFINGER.  
DR PRODOM; PD000003; Znf\_C2H2; 1.  
DR SMART; SN00355; Znf\_C2H2; 13.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 10.  
KW Transcription regulation; Activator; zinc finger; Metal-binding;  
KW DNA-binding; Repeat; Nuclear protein; LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 372 382  
FT ZINC FINGERS.  
FT ZNFING 403 777  
FT ZNFING 403 425  
FT ZNFING 434 456  
FT ZNFING 466 488  
FT ZNFING 497 520  
FT ZNFING 526 548  
FT ZNFING 554 577  
FT ZNFING 583 605  
FT ZNFING 611 634  
FT ZNFING 640 662  
FT ZNFING 668 691  
FT ZNFING 697 719  
FT ZNFING 725 748  
FT ZNFING 754 777  
SQ SEQUENCE 783 AA; 88956 MW; 1722D1C23F019DF8 CRC64;

Query Match 2.5%; Score 99; DB 1; Length 783;  
Best Local Similarity 19.2%; Pred. No. 9.6;

Matches 117; Conservative 74; Mismatches 207; Indels 210; Gaps 34;  
QY 71 TPKYDNCITLNPVKHVIADAQNTISQYACHDOAVTILSPGALGIEFLKFRVILE 130  
DB 339 TAYDNNSEI---EVQATASAMLHDESG-----GLD-----RVPKQ 374  
QY 131 ELKS---EGROCOOLIKDPKOLNSSFKFTGMSQP--FLANKFETDYFVKVVPFSTK 184  
DB 375 KSKKKRPESKOYSAIFVAPDQGT-----LRVYPCGKGRKTERFLK--RHIK 423  
QY 185 NESYHPFFETFRACDLLOPNLACKPFMKPRNLNISQSGSDMVSDHAPHNFGPREF 244  
DB 424 N-----HPEYLANKKY---HCTEDYSTNKKIS----- 448  
QY 245 YLHYKLKHBGPFKRTCKQBOTETTSCILQNVSPGDYIIELVDDTNTTRKVMHVALKP 304  
DB 449 LNHMHESH---KLTIKTEKTECCDC--RKNLSHA-----GLTCTHKTMT 490  
QY 305 HSPWAGPIPAVAITVPLVVI---SAFATLEY---VMCKQOENIYSHLDESESESTY 357  
DB 491 -----KGVNKTCKEFCDYETABQTLNHLHLVHRRK-----FPHICGCGKGRH 537  
QY 358 TAALPRE-RLRPRFVFLC-----YSSKQGN---HMNVQCFAIFLQDFCCCEVALDWE 409  
DB 538 PSALKKHIVHTGKPYEYOCEYKSADSSNLKTHIKSHKEIPLK-----CDICL--L 590  
QY 410 DFSLREGQREWI---QKTHESQFIYVCSKGMKYFVDKKNYKKGGRSGKGLFLV 466  
DB 591 TFSDTKEAQHVLHQSERTHQ-----CS-----HCNKKSSNSDLKRHTISV 633  
QY 467 AVSAIAEKLROAKQS---SSAALSKEFVAVFYDS-----CEGDVPG-----TLDLSTR 511  
DB 634 HTRAYPHKDCMCKGPHRPSLAKKHVATHKSKMHQCHDCRNSDPDFLLSHHLSAHTK 593  
QY 512 YRLMDNLPCOLSHLESRDGLQPGQHTQSGRNTFRSKRSGLYVAICNKHOFIDEEP 571  
DB 594 -----NVPEKCKCKK-----EFOOCELTGTHKTHSSRKVYQ--CEYCEYSTKDA 737  
QY 572 DWFKQFVFPHPPPLRTPVLEKFDGSLGVLDVNCVCKPSPESDFCLKVEAAVLGATGPD 631  
DB 738 SGFKRVISHTKDYPHR-----CDFCKK-----GFRPSE 768  
QY 632 -SQHESQH 638  
DB 769 KNOHMRH 776

RESULT 15  
PSUL\_YEAST  
ID PSUL\_YEAST STANDARD: PRT: 970 AA.  
AC P51550;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 13-JUN-2002 (Rel. 41, Last annotation update)  
DE mRNA decapping protein 2 (PSUL protein).  
GN DCP2 OR PSUL OR INL18C OR N1917.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RA Tzagoloff A.A.;  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=97245296; PubMed=9090055;  
RA de Antoni A.; D'Angelo M.; Dal Pero F.; Sartorello F.; Pandolfo D.;  
RA Pallavicini A.; Lanfranchi G.; Valle G.;  
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames.";  
FT



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OM protein - protein search, using sw model

```
Run on: May 6, 2003, 13:40:26 ; Search time 96 Seconds
        (without alignments)
        1616.182 Million cell updates/sec
```

**Title:** PS-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWLQCSVFETVNACLNG.....CKADLGCRSYTDDELHVAAPL 753

Scoring table: BLOSUM62

Gapop:10.0 , Gapext:0.5

Searched: 671580 segs. 206047115. residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Fast processing: Minimum Match 0% :  
Maximum Match 100%

**Listing first 45 summaries.**

**Database :**

- SP\_NREMBR\_211:
- 1: sp.archae:
  - 2: sp.bacter:
  - 3: sp.bacterin:
  - 4: sp.fungi:
  - 5: sp.human:
  - 6: sp.invertebrate:
  - 7: sp.mammal:
  - 8: sp.mhc:
  - 9: sp.organelle:
  - 10: sp.phage:
  - 11: sp.plant:
  - 12: sp.rodent:
  - 13: sp.virus:
  - 14: sp.vertbrate:
  - 15: sp.unclassified:
  - 16: sp.rvirus:
  - 17: sp.bacteriap:
  - 18: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3005	74.9	564	4	Q9UFA0 homo sapien
2	2616.5	65.2	582	11	Q8M5J8
3	1961	48.9	745	13	Q8QHJ9 brachydanio
4	1952	48.6	745	13	Q8QHJ6 brachydanio
5	170.5	4.2	846	5	Q9NA64 caenorhabdi
6	117.5	2.9	562	4	Q99755 homo sapien
7	117	2.9	757	3	Q13399 ustilago ma
8	117	2.9	917	10	Q81789 arabidopsis
9	117	2.9	2946	10	Q64634
10	116.5	2.9	901	16	Q9KE04
11	112.5	2.9	938	11	Q60669
12	112.5	2.8	549	4	Q99754
13	111.5	2.8	348	4	Q9HA60
14	111.5	2.8	370	4	Q96KN9
15	110	2.7	428	4	Q9NTU6
16	108.5	2.7	3788	11	Q922X9 rattus norv

## ALIGNMENTS

## RESULT 1

RESULT 1	Q9UFQAO	PRELIMINARY	PRT; 564 AA.
AC	Q9UFQAO		
ID	Q9UFQAO		
CD	Q9UFQAO		
DT	01-MAY-2000	(TREMBrel. 13, Created)	
DT	01-MAY-2000	(TREMBrel. 13, Last sequence update)	
DT	01-MAY-2000	(TREMBrel. 13, Last annotation)	
DE	Hypothetical 63.1 kDa protein (Fragment).		
DE	Hypothetical 63.1 kDa protein (Fragment).		
DE	DKFZF0434N1928		
OS	Homo sapiens (Human).		
GN	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Hominoidea; Hominidae; Homo		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo		
OX	NCBI TaxID=9606;		
OX	NCBI TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=TESTIS;		
RC	Blotter K., Boecher M., Brandt P., Mewes H. W., Wiemann S.;		
RA	Submitted (NOV-1999) to the EMBL/GenBank/DBJ		
RA	EMBL; AL133097; CAB61408.1;		
DR	Hypothetical protein.		
DR	Hypothetical protein.		
DR	NON_TER		
DR	NON_TER		
FO	SEQUENCE 564 AA; 6B3AA3BD4523E		
FO	SEQUENCE 564 AA; 6B3AA3BD4523E		

Query Match 74.9%; Score 3005; DB 4; Length 564;  
Best Local Similarity 99.8%; Pred. No. 1.2e-266;  
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

190	HPPEFFTRACOLLLOPONTACKPFKPKRNLAISQSGDSQVSDHAPHNPFGRFFYLHYK	249
QY		
DB		
1	HPPEFFTRACDCLLOPONTACKPFKPKRNLAISQSGDSQVSDHAPHNPFGRFFYLHYK	60
DB		
250	LKHEGPFKRKTKCQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVHSPPWA	309
QY		
DB		
61	LKHEGPFKRKTKCQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKEVISPWA	120
DB		
310	GPRAVAITPLVLIWSAFATLFTVCKRKKQENIYSHLDESSESTTAAALPRRLRPR	369
QY		
DB		
121	GPRAVAITPLVLIWSAFATLFTVCKRKKQENIYSHLDESSESTTAAALPRRLRPR	180
DB		

```

QY 370 PKVELCYSSKDGQNMVYOCFAFLQDPCCEVALDIADEFSLCREGQENVIQIHES 429
Db 181 PKVELCYSSKDGQNMVYOCFAFLQDPCCEVALDIADEFSLCREGQENVIQIHES 240
QY 430 QFIIVVCSKGMKYPVDKNNKKGKGGSGKGLFLVAVSAIAELKRAQSSAALSFP 489
Db 241 QFIIVVCSKGMKYPVDKNNKKGKGGSGKGLFLVAVSAIAELKRAQSSAALSFP 300
QY 490 IAVYDYSCGDVPGILDISTKYRLMDNLPOLCSHLSDHGLQSPQHTROGSRNRYER 549
Db 301 IAVYDYSCGDVPGILDISTKYRLMDNLPOLCSHLSDHGLQSPQHTROGSRNRYER 360
QY 550 SKSGSLVAICNNHOFIDEEPWFKEQFVFPHPPLRYRZPVLKEDSGLVLDVYKGP 609
Db 361 SKSGSLVAICNNHOFIDEEPWFKEQFVFPHPPLRYRZPVLKEDSGLVLDVYKGP 420
QY 610 GPESDFCLKVEAAVLGATGPADSPQSHQSGGLQDGEAPALDGSAAALQPLHTVYKAGSP 669
Db 421 GPESDFCLKVEAAVLGATGPADSPQSHQSGGLQDGEAPALDGSAAALQPLHTVYKAGSP 480
QY 670 SDMPDGSGLYDSSVPSSELSPLMGLSTDTQETSSILTESVSSSGSLGEEBEPALPSSKLL 729
Db 481 SDMPDGSGLYDSSVPSSELSPLMGLSTDTQETSSILTESVSSSGSLGEEBEPALPSSKLL 540
QY 730 SSGSKADLGCSTYTDLHVAAPL 753
Db 541 SSGSKADLGCSTYTDLHVAAPL 564

RESULT 2
Q8R5J8 PRELIMINARY: PRT: 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (T:EMBLrel. 21, Created)
DT 01-JUN-2002 (T:EMBLrel. 21, Last sequence update)
DE Similar expression to FGF protein (fragment).
GN Sef.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=21802165; PubMed=11802165;
RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signalling."
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL: AF424804; AAL79530.1;
FT NON-TER
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 65.2%; Score 2616.5; DB 11; Length 582;
Best Local Similarity 84.6%; Pred. No. 5.6e-231;
Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

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QY 171 TDYFKVVPFPIKSNESNHPFFETRACOLLQONLACKPFRNLTISQSGSDMOV 230
Db 1 TDYFKVVPFPIKSNESNHPFFETRACOLLQONLACKPFRNLTISQSGSDMHV 60
QY 231 SFDHAPNFGPRFFHYLKLKHEGFRKTKQBOYTETTSCLQNSPGDYIIELVDDT 290
Db 61 SFDHAPNFGPRFFHYLKLKHEGFRKTKQBOYTETTSCLQNSPGDYIIELVDDT 120
QY 291 NTRKRWIYALKPVHSGWAGPRAVAITVPLVWISAFATLFTVWCRKKQENIYSHLDE 350
Db 121 NTRKRWIYALKPVHSGWAGPRAVAITVPLVWISAFATLFTVWCRKKQENIYSHLDE 180
QY 351 SSESSTYTAALPRRLRPKPVFLCYSSKDGQNMVYOCFAFLQDPCCEVALDIADEF 410
Db 181 SSESSTYTAALPRRLRPKPVFLCYSSKDGQNMVYOCFAFLQDPCCEVALDIADEF 240

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```

QY 411 FSLCEGOREWYLOKIHESQFIIVVCSKGMKYPVDKNNKKGKGGSGKGLFLVAVSA 470
Db 241 FSLCEGOREWYLOKIHESQFIIVVCSKGMKYPVDKNNKKGKGGSGKGLFLVAVSA 300
QY 471 IAEKLRQAKSSAALSFPVYDYSCGDVPGILDISTKYRLMDNLPOLCSHLSDHSDH 530
Db 301 IAEKLRQAKSSAALSFPVYDYSCGDVPGILDISTKYRLMDNLPOLCSHLSDHSDH 357
QY 531 GLQEPF-COHTROGSRNRYERPRKSGSLVAICNNHOFIDEEPWFKEQFVFPHPPLRYR 589
Db 358 GLQEPF-COHTROGSRNRYERPRKSGSLVAICNNHOFIDEEPWFKEQFVFPHPPLRYR 417
QY 590 EPLVLEKDFSGLVLDVYKGPESDFCLKVEAAVLGATGPADSPQSHQSGGLQDGEA 647
Db 418 EPLVLEKDFSGLVLDVYKGPESDFCLKVEAAVLGATGPADSPQSHQSGGLQDGEA 477
QY 648 RPAIDGSAAALQPLHTVYKAGSPDMPDGSGLYDSSVPSSELSPLMGLSTDTQETSSIL 707
Db 478 RPAIDGSAAALQPLHTVYKAGSPDMPDGSGLYDSSVPSSELSPLMGLSTDTQETSSIL 537
QY 708 ESVSSSGSLGEEBEPALPSSKLLSGSKADLGCSTYTDLHVAAPL 753
Db 538 ESVSSSGSLGEEBEPALPSSKLLSGSKADLGCSTYTDLHVAAPL 582

RESULT 3.
Q8RQJ9 PRELIMINARY: PRT: 745 AA.
AC Q8RQJ9;
DT 01-JUN-2002 (T:EMBLrel. 21, Created)
DT 01-JUN-2002 (T:EMBLrel. 21, Last sequence update)
DE Sef.
GN Sef.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21824236; PubMed=11802164;
RA Tsang M., Friesel R., Kudoh T., Dawid I.;
RT "Identification of Sef, a novel modulator of FGF signalling."
RL Nat. Cell Biol. 4:165-169(2002).
DR EMBL: AF364103; AAL76112.1;
SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;

Query Match 48.9%; Score 1961; DB 13; Length 745;
Best Local Similarity 51.4%; Pred. No. 1.1e-170; Indels 58; Gaps 10;
Matches 390; Conservative 114; Mismatches 197;

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```

QY 1 MAPWQLQCSVFFTVNACLSGOLAAVAGSGRGARGADTCGWRMKAARPRCLVANEVGP 60
Db 7 LAHFEMASCLFLCYTASVNG-----GKRGNSDKCYK-----OGTQT 43
QY 61 ASRSGSL--YNITFKYDNTTYLVGVKHVIAQAQNTTISQVACHQVAVTILWSPGALG 118
Db 44 SSMDEGARKLVGTVFTRDNCVNMNPLGKHAIHEVNNITFSLHSCDSQAAYVHVHNASPLG 103
QY 119 IEFLKGRVTELEKSESGKQCOOLLKDPKQANLSPFKTGMESOPFLNMFETDYEKVV 178
Db 104 IEHVGFRVYLEDKNEPKQCOHLLKDPQLNFKYKTKRMSSQPFSLAFEDYWRIV 163
QY 179 PPSKIKNESNHPFFETRACOLLQONLACKPFRNLTISQSGSDMOVSDHAPN 238
Db 164 PEPFELNDSEFPFSLRTNSCEVLLGPDNLVCPFPKPKRLNLSQGLNSHVVFDHAPST 223
QY 239 FGFREFFLHYLKLKHEGFRKTKQBOYTETTSCLQNSPGDYIIELVDDTNTTKYMH 298
Db 224 FGFESIYLYLKLKHEGFRKTKQBOYTETTSCLQNSPGDYIIELVDDTNTTKYMH 283

```



Best Local Similarity 21.4%; Pred. No. 2.5e-06;  
Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

QY 99 QYACHDVAVILMSGALGIFELAGFVLEELKSGRCQOOLILKDPKOLNSPKRFG 158  
Db 294 QY-CFEVEYRLDSS---GIVMLASAIITDELRLTE-----INGRVOFGEF----- 338  
QY 159 NESOPFLANKETDYFVKVPPPPSTKESNHYHFFETRACDLLOPNLAC-KPWKPR 217  
Db 339 ---NFTDIELDTLIPSVIPESAH-----GRC-LCVTENGSCSLAAQWKEV 382  
QY 218 NLMSHQSDMOVDFRAPHNFGFFYLHYLKHGPKFRKTKQBOETTETSCLLQNV 277  
Db 383 KLT-----RIEKPATSN-----QTESDKAKEDKEDTTT----- 415  
QY 278 SPGDYIIELVDDTNTTKVNH-YALKPVHSPWAGPIRAVAITVPLVLSAFATL--FTVM 334  
Db 416 -----WHTVA-----ITGGAILAILFSLVCAGLKCKKF 445  
QY 335 CREKQENIYSHLDESESESTYTAALPRERLRPRKPVLCYSSKQGNHNVYQCFAYP 394  
Db 446 NKKKASNI--HLLNEPAPS-HSGSIFL-TLKQSTISVLIVT-SHDSAQHEAAVLAFEL 500  
QY 395 LQDFQCEVALDMEFSLCREGORENWIQIHESOFIIVVCSKGMKYFDKKNYKHGG 454  
Db 501 LRDVFLNVLHLOWDEODI--ENRABYNSSIVRANKVLIINSIG-AYF--RTVFRHOR- 555  
QY 455 GRGSGKGEFLVAVSAIAELKQAKQSSAALSXFIATVFDYSCEDV--PGILDLSKY 512  
Db 556 -----EPAIERTITGRND-----VIFDMOCELALQHPVCISCHFSY 591  
QY 513 -----RLMD-NLPOLCSHLSDHGLQPPGQHTROGSRNRYPRSKSGSLYVAI 560  
Db 592 TNPKYVFFPINLLQYISIP--NSLMTWTALTQPARPEQLAGFNQYFAR---LQAI 644  
QY 561 CNMHQFIDEEDQWEK-----QVFFHPPELYR----- 589  
Db 645 SRLNLYESDFQWENTHVRATRRVSELEAHNIVPL-PPSLEVVEDAFQOMETLPI 703  
QY 590 EPVLEKF-----DSGLVNDVMCKPGESDCLKVEAAVIGATGPADSOHES 636  
Db 704 DELKEFAAKDELVEVLDESVDKLEEDVKCAPG-----IHVEPEVLEPAEPPME 758  
QY 637 QHGLDQDGEARPAIDGSA-----LOPLL-HTVKAGSPDMPRDSCIYDSS-VPSSELS 689  
Db 759 AED-DEEDDDVDSVEGOTARIEELQRLIVH-----KDMNEDSGNLDYAVYSGSDFS 809

RESULT 6  
QY9755 ID Q99755 PRELIMINARY; PR: 562 AA.  
AC Q99755  
DT 01-MAY-1997 (Tremblrel, 03, Created)  
DT 01-MAY-1997 (Tremblrel, 03, Last sequence update)  
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)  
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97115834; PubMed=8955136;  
RA Lojens J.C., Anderson R.A.;  
RT "type I phosphatidylinositol-4-phosphate 5-kinases are distinct  
RT members of this novel lipid kinase family";  
RL J Biol Chem 271:32937-32943(1996).  
DR EMBL: 078576; AAC50911.1;  
DR InterPro: IPR002498; PIP5K.  
DR Pfam: PF01504; PIP5K; 1.  
DR SMART: SM00330; PIP5K; 1.  
KW Kinase; Transferase.

50 SEQUENCE 562 AA; 62633 MW; A8F7988EB73506A0 CRC64;  
Query Watch 2.9% Score 117.5; DB 4; Length 562;  
Best Local Similarity 18.1%; Pred. No. 0.098;  
Matches 133; Conservative 105; Mismatches 239; Indels 257; Gaps 35;  
QY 53 VANEGVGPAKNSGLNITFKYDCTT-----YLMVGVKRVIAQONITISYACHDOV 106  
Db 1 MASASGSS--SVGFSFDPVPSCTSSAASGIKRPMASEVLEARDQSTISLV----- 53  
QY 107 AVTILMSGALGIEFLK-GFRVILEELKSGRCQOOLILKDPKOLNSPKRKTGMSQPL 165  
Db 54 -----PYASGMPKIKIGHRSDVSSGETTYKKTSSALKGAIOGITHVVGSLTKPR 106  
QY 166 NKKFETDYFVKVVPFSS-----IKNESNYHFFETRACDLLOPNLACRPFKPRNLI 221  
Db 107 DVLMDFTVYVESIFFPSEGSNLTPAHYNDREKTYA----- 143  
QY 222 SQHSDMOVDFRAPHNFGFR--FFY-----LHYKLKHGSPKRT 260  
Db 144 -----PVAFRFRFELGIRPDVLYSLSEPLIELSSGASGLY-VSSDDREIKT 195  
QY 261 CKBQOTTETSCLLQNVSPGYIIELVDDTNTTKVNHYALKPVHSPWAGPIRAVAITVP 320  
Db 196 VQHKAE-----FLQKLLPGYTM-----NLNQN-----P 219  
QY 321 LVVISAFATLFTVMCRKQ-----QENIYSHLDESESESTYTAALPRERLRPR 370  
Db 220 RTLLPKFGLYCYOAGKNIIRIVVNNLLPRSVKMHKYDLKSGSTYKRRASQEREKPLP 279  
QY 371 KVFCLYSSKQGNHNVVOCFAVFLQDF-CGCEVALDMEFSLCREGORENWIQ--KI 426  
Db 280 -----TFKD-----LDLQIDPDGLFDADYN--ALCKTLQRDCLVLOSFKI 320  
QY 427 HESQFIIV-----CSGKMYFVDKKNYKHGGSGSGKGEFLVAVSAIAELR 476  
Db 321 MYSILMSIHNDIADQREPLSSEYQYSDYR-----RPAQKALYSTAMESIOGEAR 372  
QY 477 Q-----AKQSSAALSXFIATVFDYSCEDVPGILDLSKTKRLMDNLPQLC 522  
Db 373 RQGTMTDDHMGGIPARNKGERLLLYI-----GLIDILQSTRFVKKLEHWS 419  
QY 523 SIL-HSRDH-GLQEPQHTROGSRNRYPRSKSGSLYVAICNMHQFIDEEDPWFQFVP 580  
Db 420 KALVHDGDTVSVHRPGFYAERFOR-----FMCH-----TVFKK--IP 454  
QY 581 FHPPLRYREPVLEKFDGLVNDVMCKPGESDCLKVEAAVIGATGPADSOHESQHG 640  
Db 455 LKPSPSK-----KFRSG--SFSRRAGSGNSCITTOPSVSG-----EHKAQ---- 494  
QY 641 LQDGEARPAIDGSAALOPLLHTVKAGSPDMPRDSCIYD-----SSVPSSELSLPLEGL 696  
Db 495 -----VTKAEVEPCVH--LGRPDVLPQTPLEISEGSPIDPSFS-PLV-GE 539  
QY 697 STDQETSSLTESY 710  
Db 540 TLQMTTSTTLEKL 553

RESULT 7  
QY13399 ID Q13399 PRELIMINARY; PR: 757 AA.  
AC Q13399  
DT 01-JAN-1998 (Tremblrel, 05, Created)  
DT 01-JAN-1998 (Tremblrel, 05, Last sequence update)  
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)  
DE Telomere-associated recQ-like helicase (fragment).  
GN UTASHECQ.  
OS Ustilago maydis (Smut fungus).  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=5270;  
RN [1]

RP: SEQUENCE FROM N.A.  
RC STRAIN:FR2;  
RA Saucha-Alonso P., Guzman P.;  
RT Organization of chromosome ends in *Ustilago maydis*: recO-like  
RT Helicase motifs at telomeric regions;  
RL Genetics 0:0-0(1998);  
DR EMBL: AF010885; AB95264.1;  
DR EMBL: AF010885; AB95264.1;  
DR InterPro: IPR001410; DEAD;  
DR InterPro: IPR001650; Helicase\_C;  
DR Pfam: PF00270; DEAD; 1;  
DR Pfam: PF00271; Helicase\_C; 1;  
DR SMART: SM00490; HELIC\_C; 1;  
DR ATP-binding; Helicase;  
FT NON\_TER;  
SQ SEQUENCE 757 AA; 84382 MW; 1AE1EA144353837 CRC64;  
Query Match 2.98; Score 117; DB 3; Length 757;  
Best Local Similarity 20.48; Pred No. 0.17;  
Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;  
QY 268 ETTSCLLQWVSGDIIIEVDNTRKVMHVALKVPWAGPIRAV-----ATVPL-- 321  
DB 77 ETTILPTVALRANNAKLQVNN-----IRYVWQP-GSKAAPIVLYSTEAATLAFKE 131  
QY 322 -----VVISAFATFTVCRKKQOENIYSHLDESESSSTYTAALP----- 362  
DB 132 YANLLQOQRLDRIVIDCHLTLTARSTYRSMNOLAHVRDVTQVTLTLPPIPEDA 191  
QY 363 -----RERLRPRKVF-----LCYSSKQGNHNVVQCF-ATPLQDFCCEVALDLWEDF 411  
DB 192 FISHNKLTPLVRESTNRSNLCYSVRTAEHRMSGTCYDAVRVD--ECRARTDIW--- 246  
QY 412 SLCSGORENVIQKIHESQFTIVVCSKGMKVFVK-----ANYKKGGRGS----- 458  
DB 247 -----NGORD-----RIIVYCHS--KELYARLAEMLGCAAYSESSEADKAALIQ 290  
QY 459 -----GGEFLVAVSAIAEKURQKSSAALSKFIAYVYDSCGVDPGIL--DLSTKY 512  
DB 291 DWIGKGSVPVYATSA-----LVGDFDIYHVFYHLLGPDGLDTDF 331  
QY 513 -----RLMDNLPCLGSHLHSDRHGLQEPQOHTROGSRNFRFS 550  
DB 332 SQESGRAGRGMPAESILLAGPOLDDRAP-ASGRASSAEKGVAPG--ADKEAMQLYRS 387  
QY 551 KSGRSLYVAICNHQFIDDERPWFKEQFVFPFPPPLRYREPVELEKEDSLVNDVMCKPG 610  
DB 388 RK-----YCLRGVLSQLQDSM-----RWCEGDLCSVC 419  
QY 611 PESDFCLKVEAAVLGATGPAQDSOH-----ESQHGGLDQCEARPALDQSAALQPLHTVKG 667  
DB 420 PCHHF-----QARGPGQDQFTAPAGADPSTQGRHPSNHGSS--HPSMH----- 463  
QY 668 SPDMPRDSGIVDSVPSE-LSLPLMEGLSDQDTSTSSUTESVSS-----SLGEEPPPA 723  
DB 464 -----GSSHPSSGSHPSIHGSSHPSSIHGSS-HPSIHGSGHGGORRKKQPD 510  
QY 724 LPSK 727  
DB 511 PPSE 514  
RESULT 8  
ID 081789 PRELIMINARY; PRT: 917 AA.  
AC 081789;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 101.6 kDa protein.  
GN F8D20.70 OR AT4G35560.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosida II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN  
RP SEQUENCE FROM N.A.  
RA Koetter P., Hempel S., Entian K.-D., Hoheisel J., Jesse T.,  
RA Heljnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).  
DR EMBL: AL031135; CAZ0026.1;  
DR EMBL: AL161587; CAB0272.1;  
DR InterPro: IPR001680; WD40;  
DR Pfam: PF00400; WD40; 2;  
KW Hypothetical protein; Repeat; WD repeat.  
SQ SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;  
Query Match 2.98; Score 117; DB 10; Length 917;  
Best Local Similarity 18.38; Pred No. 0.23;  
Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps 42;  
QY 19 NGSOLAVAGSGRAGADTCGRM--KAAARPR--LCVANEGV----- 58  
DB 92 NGSRSV-----GYSNG-DILLMSIDSKGCESSAMICKMLGVKSEKIPASLAKWY 145  
QY 59 -GPASR-----NSGLNTEFKYDNCITLNPVKHV---IADAONI--TISOYACHQ 105  
DB 146 AGRASRYTVSSNSLQVLLNQTETRMILKHLRVSFPCADMEHIAVDSQSKHQ 205  
QY 106 VAVTILWSPALGI--EFLKGRVILLELKSQROCOOLIKDPKOLNSFFRTGMSQP 163  
DB 206 DFLVFLGKGRVAYDDYMEKYLQSQSKSPSPKPKVTKLPFDSSSITVCKFLTP 265  
QY 164 -FLANKFTDY-----FKVVPFPPSIRKNSN---YHPFF-----FTRACOLLQPD 206  
DB 266 SHLLNLSDE-DYAOALAKDAVFPFLPFTVPKESRSHAPGFTKVKVYITGHCGTISV 324  
QY 207 NLACK-----PMPKR-NLANSOG-----SDMOVSEFHAPHNCFEFLHY 248  
DB 325 DMTCSPILVLELKBQIDQDVSSRGNALTAHLSDNSRLYSGLDNGHGVLYRKEPEY 384  
QY 249 KLKH-----EGPFR-----KTCQQTETTSCLLQVSP-----GDYIELV 287  
DB 385 LTENSTPFGSLKGNHIVQSVYKIKUTGTCIKQSNKSHLAGSDQGHSLVEVI 444  
QY 288 DDNTTTRKVMHVALKVPWAGPIRAVAITVPLVVISAFATLT----- 332  
DB 445 D-----ALTPV-----LVSLVDIEEANVLYTKHIASDICGIIISLQ 482  
QY 333 -----VMCRKQOENIYSHLDESESSSTYTAALPRERPRPKPVFLCYSKD 380  
DB 483 FESCIVQGEKVLVAVRDSVFA-LDSDTGNMIGTNMKPK-----KPEKVLVMOILD 536  
QY 381 GQHNHNVQCFAYFLQPCGCEVALDLWEDSLCSGORENVIQKIHESQFTIVVCS-- 437  
DB 537 GK-----QDTSG-----NGFTSRES-----TVEEISIQPSVLVSEKA 571  
QY 438 -----KMKYFVDKKNYKHG-----GGRSGKGLFLVAVSAIAE-----X 474  
DB 572 IYIYSLAHVVGKVKVLRKFKSSSPICSAFTGTSGVG---LTVFDGTGVIRESLPE 628  
QY 475 LRAQKQ-----SSAALSKFIAYVFDYDSCGD-----VPGTDLSTKYRLMD 516  
DB 629 LSLQKTSIRGTYSPPKNSLPETITIASNDGDLVWVNGDELIVSSVLPQKTEPLVE 688  
QY 517 NLQCLSHLSHSDHGLQEPQOHTROGSR-----NYERSKGRSLYVAICNHQFIDE 570





RP SEQUENCE FROM N.A. 9153;  
 RC STRAIN-C-125 / JCM 9153;  
 RX MEDLINE-20512583; PubMed-11058132;  
 RA Takai H., Nakase K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fujii F., Hirano C., Nakamura Y., Ogasawara N., Kohara S.,  
 RA Horikoshi K.,  
 RT Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.\*;  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY  
 CC (ABC TRANSPORTERS).  
 DR EMBL: AF001510; BAB04773.1;  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_transporter.  
 DR InterPro: IPR002559; Transposase\_11.  
 DR Pfam: PF000005; ABC\_tran.1;  
 DR Pfam: PF01609; Transposase\_11.1;  
 DR ProDom: PD000006; ABC\_transporter.1;  
 DR SMART: SM00382; AAA.1;  
 DR PROSITE: PS00211; ABC\_TRANSPORTER.1;  
 DR ATP-binding; Transport; Complete proteome.  
 KW ABC-binding; Transport; Complete proteome.  
 SQ SEQUENCE 901 AA; 104585 MW; 451940650B2CBB CRC64;  
 Query Match 2.9%; Score 116.5; DB 16; Length 901;  
 Best Local Similarity 19.6%; Pred. No. 0.25;  
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;  
 QY 61 ASRNSGLNITFYDNCCTTLPVGVKVIADQNITISQY-ACHDOVAVTILMSPGALGI 119  
 DB 333 ALKESGL-----PLPKTLIADAGYSESNTYVMADELFTLIPS----- 371  
 QY 120 EFLKGVRIIEELKSGR-----CCQOL--ILKDPQLNSSFKECTGMSOPFLNMF 169  
 DB 372 ---HFR--QDQRSFAKRPHPYWRCDDEDDVYCPNQKRVFKYTRTDYV---GY 423  
 QY 170 ETDYFV-----KVPP-PSI-----KNESNYHFFFRACDILLQPDNLACKPFWKPR 217  
 DB 424 ARDFVYECSCGCPFPECTKARGNQVHPYV-----EELKAKQHKLK 471  
 QY 218 NINISONG-----SDMOVSDPHAPNFGFFPYLHVYKLGHEGPFKRTCKQQTET 269  
 DB 472 ---SEERTLYOKRRTDVSFVGHVQNLGFRLLRGK----- 507  
 QY 270 TSCILLQVSPGVIIELVDVTNTRKVMHVALKPVHSPWAGPIRAVAITVPLVLS-AFA 328  
 DB 508 -----ESVHIELGLVALAHNR 524  
 QY 329 TLPTVMCRKKQENIYSHLDESSESSTYTAALPRERLPRKVFYLCYSKQGNHNVV 388  
 DB 525 KRATVDRSREPTNQHNRN-----RIKRP-----SRFTVL 558  
 QY 389 QCF---AYFLQDCCGCEVALDWEFSLCREGREW---IQIHESQFIIVVCSGKHK 441  
 DB 559 ECFMDSFFFKDSQGYASFALED--KLREGGENNIEVDLSKTYNRQV---KGIN 612  
 QY 442 YFVKYKIKHGGRSGGSGELFLVAVSAI-----AEKLRQAKQSSAALSK 488  
 DB 613 NPIEKGEVGLGPNAGKSTTISMISLIPTSGDVILKGSITHKOSKAIRSILGVQ 672  
 QY 489 FLAVFDYSC-----GDVPCILDLSTKYRLMDNLPOLCSHLSDRGLOEQGHTRQG 542  
 DB 673 EIAVYHDLTARENLAFFGIYGLGEELKUR-NESTLQIV-----GLEE-----RQN 718  
 QY 543 SRNRYFSKSGSLYVACNMHQ---FIDEPE 571  
 DB 719 DRVHTFSGMKRNLNIAVALLPELIMDEP 750  
 RESULT 11  
 ID Q60669  
 AC Q60669 PRELIMINARY; PRT; 938 AA.  
 DT 01-NOV-1996 (TRENDEL. 01, Created)

DT 01-NOV-1996 (TRENDEL. 01; Last sequence update)  
 DT 01-JUN-2002 (TRENDEL. 21; Last annotation update)  
 DE Protein kinase (Fragment).  
 GN EPHB3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95200798; PubMed-7893599;  
 RA Ruiz J.C., Conlon F.L., Robertson E.J.,  
 RT Identification of novel protein kinases expressed in the myocardium  
 RT of the developing mouse heart.\*;  
 RL Mech. Dev. 48:153-164(1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 DR EMBL: U11493; AAA67925.1;  
 DR HSP: P29323; IB4F.  
 DR MGD: MGI:104770; Ephb3.  
 DR InterPro: IPR001090; Ephrin\_receptor.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003962; FniII\_repeat.  
 DR InterPro: IPR003961; FN.III.  
 DR InterPro: IPR001660; SAM.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR InterPro: IPR001436; Ykase\_receptorV.  
 DR Pfam: PF01404; EPH\_lbd.1;  
 DR Pfam: PF00041; fn3.2.2;  
 DR Pfam: PF00069; Pkinase.1;  
 DR Pfam: PF00536; SAM.1;  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase.1;  
 DR ProDom: PD001495; Ephrin\_receptor.1;  
 DR SMART: SM00060; FN3.2;  
 DR SMART: SM00454; SAM.1;  
 DR SMART: SM00219; TYRG.1;  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1;  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM.1;  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1;  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V.1;  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V.2.1;  
 KW Glycoprotein; kinase; phosphorylation; Receptor; Repeat;  
 KW Transmembrane; tyrosine-protein kinase.  
 FT NON\_TER 1  
 SQ SEQUENCE 938 AA; 103997 MW; 8D128CA46F19E73F CRC64;  
 Query Match 2.9%; Score 115.5; DB 11; Length 938;  
 Best Local Similarity 19.4%; Pred. No. 0.33;  
 Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;  
 QY 9 SVFTFVACI-NGSOLAVA---AGSGR---ARGADTCGRMKAAAPRLC----- 52  
 DB 170 SLVTPACIACIANAVEVSVPLKLYCNGDGMVPGACATCATGEPAAKESQCRACPPGSY 229  
 QY 53 VANGVCPA-----SRNSG-----LYNIFKYDN-----CTTYLNPVGFHVTADAQ 93  
 DB 230 KAKQGEFCPLPCPNSTRTSPAAICHTCHNNFYRADSDSADSTRSP-PRGVLISN- 287  
 QY 94 NITISYACHDOVAVTILMS-PGALGTFELKGRVILBELK-SEG-----RQCOOLIL 144  
 DB 288 -----NETSLILESEPRDLGGDDLLNYVICKKRCRGSSGAGGATPCSRCDNVE 337  
 QY 145 KDPQLNSSEKRTGMSOPFLNMFETDYEVKVVPPSPISKNESNYHFFFRTRACDILLQ 204  
 DB 338 FVPRQLGLTERRVHIS-----HLLAHTRYTFEQAVNGVSGKSLPPRYAAVNITNQA 392  
 QY 205 PDNLACKPFWKPNLNIHQSGDMQVSDHAPHNFGFFPYLHVYKLGHEGPF-KKTKCK 263

Db 393 PSEV-----PTLHSTSGSLSLWPPERNG---VILDYEMK---FEKSKAIAS 439  
 Qy 264 EOTTETTSCLLQVSP-GDYIIELVDDNTRKV-----MYALKPVHSPWAGPTRA 316  
 Db 440 TVTSKNSVQLQGLQDARVYQV-----RAKTVAGYGYTHPAEFETTSERGGAQQLQ 494  
 Qy 317 ITVPLVWISAF-----TLFTVNCRKQOENIYSHLOESSSESYTAALPRELR 368  
 Db 495 EQLPLVGSNAGVFPVWVWIALVCLRKORH-----GPDABYTEKL-QOYIAP 543  
 Qy 369 RKVFLCYSSDQGNHNVVQCFAYFLQDFC-GCEVALDLWEDFSLCREGQEWV 427  
 Db 544 GNVKVIDPTEYEDPN-EAVREFAKEIDVSCVKEIEVIGAGEVGCVR-----589  
 Qy 428 ESOFIIVCSGKMYFDVKKNYKHGGGSGKGLFVWASAI-----AEKLRQAKOSS 483  
 Db 590 -----GRLLKPGREVF-VAIKTLAVGVTQRQEDFLSEA 623  
 Qy 484 AALSKEIAYDYSCEDVPGILDLS---TKYR-----LMDNLPOLCSHLHSRDLQ 533  
 Db 624 SNGQF-----DHPNIRLEGVTVKSRPMILTFEWC-ALDSFLRLND-----667  
 Qy 534 EPGQHT-----ROGSRNY-FRSKGRSLY---AIC-----NNHQFIDE 569  
 Db 668 --GOFTVQLVGLRGTAAGMYLSMNYVHRDLAARNILVNSLVCKVSDFGLSRFLSD 725  
 Qy 570 EPDMFEKQF-----VPFH---PPPLRYREPVELEKFS-----GLVLDNVCKPQPE 612  
 Db 726 DPS--DPTTYSLLGKIPINWAPPIAYR-----KFDASDQWISYGVNNEVMS-----773  
 Qy 613 SDPCLKVEAAVLGATGADPSOHSQHGGLDQGEARPDALDGAALQPLHTVKGSPSDM 672  
 Db 774 -----YGRQPVNMSNGDINAVEQDYELPPMDCTALHQLMASCVVRDNL 822  
 Qy 673 PRDSGIYD-----SSVPSSELSPLMEGLSTDOT 701  
 Db 823 PRFSQIVNTLKLNRNAAASKVTASAPG-MSQPLIDRVVPTT 865

RESULT 12  
 Q99754 ID Q99754 PRELIMINARY; PRT: 549 AA.  
 AC Q99754;  
 DT 01-MAY-1997 (TRENBLrel. 03, Created)  
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68)  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97115834; PubMed=8955136;  
 RA Lojens J.C., Anderson R.A.;  
 RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct  
 members of this novel lipid kinase family."  
 RL J. Biol. Chem. 271:32937-32943(1996).  
 DR EMBL; U78575; AAC50910.1;  
 DR InterPro; IPR002498; PIPSK.  
 DR Pfam; PF01504; PIPSK; 1.  
 DR SMART; SM00330; PIPK; 1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 549 AA; 61186 MW; 7CD48BFEL7556AA0 CRC64;

Query Match 2.88; Score 112.5; DB 4; Length 549;  
 Best Local Similarity 18.18; Pred. No. 0.27;  
 Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32;  
 Qy 114 PGALGIEFLK-GFRVILEELKSGROCOOLIKDQKQINSFKRTGMSOPFLMKFETD 172  
 Db 41 PYASGMPFKKICHSVDSGGTYTKTTSALKGAIQIGTHTVTSLSLTKPKPDVLMQDF 100

Qy 173 YKVVVPPPS-----IKNESNYHPFFETTRACDLLQLQDNLACKPFWKPRNLNISQHSMD 228  
 Db 101 YVVISIIFPSEGNLPPAHYNDPRKTYA-----LHYKLAHEGPPFKTCQEQTT 130  
 Qy 229 QVSDPHAPHNGFR---FFY-----LHYKLAHEGPPFKTCQEQTT 267  
 Db 131 PVAFRYFRELFGIRPDYLYLCSEPLIELCSGASGLFY-VSSDDEFIKTVQHKAE 189  
 Qy 268 ETTSCILQNVSPGDYIIELVDDNTRKVHYALKPVHSPWAGPTRAIVTVPLVWISAF 327  
 Db 190 -----FLQKLLPGIYM-----NLNQN-----PRTLLPRT 213  
 Qy 328 ATFLFWCRRKQ-----QENIYSHLDESSSESYTAALPRELRPREKVFCLYS 377  
 Db 214 YGLYCVQAGKNIRIVVMNLLPRSVKMKIKYDLKSTYKRRASQKREKPLP-----T 267  
 Qy 378 SKDQGNHNVVQCFAYFLQDF-GCEVALDLWEDFSLCREGQEWVIO---KHESOPTI 433  
 Db 268 FKD-----LDLQADIPDGLFLDADMYN-ALCKTLQROCLVQLQSFKIMDYSLIM 314  
 Qy 434 VV-----CSKMYTFVDKKNYKHGGGSGKGLFVAVSAIAEKLRQ-----477  
 Db 315 SIHNDIDHAQREPLUSSTOYSVDTN-----RPAQKALYSTAMESIQGEARGGTMET 366  
 Qy 478 -----AKQSSAALSKEIAYDYSCEDVPGILDSTKYRLMDNLPOLCSHL-HSR 528  
 Db 367 DBHMGIGIPARNSKGEILLIY-----GIIDILQSYRFVKKLEHSHKALVHDG 413  
 Qy 529 DH-GLQEPQGITQSGSRNNYFRSKGRSLYVAICNNHQFIDEPDMFEKQFVFPHPPLR 587  
 Db 414 DTVSVHREPGFYAERFOR-----FMCN-----TVFKK--IPLKPSK 448  
 Qy 588 YREPVELEKFSGLVLDNVCKPESDPCLKVEAAVLGATGADPSOHSQHGGLDQGEAR 647  
 Db 449 -----KFRSG---SSFERRAGSSGNCITYQPSVSG-----EHKAO-----481  
 Qy 648 RPAIDGSAALQPLHTVKGASPSDMPDSGIYD-----SSVPSSELSPLMEGLSTDOT 703  
 Db 482 -----VTTKAEVPGVH---LQRPDLVLPQPPLEISSECSIPDPSES-PLV-GETLQMLT 533  
 Qy 704 SLSIESV 710  
 Db 534 STLEKL 540

RESULT 13  
 Q9H460 ID Q9H460 PRELIMINARY; PRT: 348 AA.  
 AC Q9H460;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE BA425A6.2 (Similar to connexin) (Fragment).  
 GN BA425A6.2.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Heath P.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL121749; CAC10186.1;  
 DR InterPro; IPR000500; Connexin.  
 DR Pfam; PF00029; Connexin; 1.  
 DR PRINTS; PR00206; CONNEXIN.  
 DR SMART; SM00037; CNX; 1.  
 DR PROSITE; PS00407; CONNEXINS\_1; 1.  
 DR PROSITE; PS00408; CONNEXINS\_2; 1.  
 FT NON\_TER  
 SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;

Query Match 2.8%; Score 111.5; DB 4; Length 348;  
 Best Local Similarity 28.9%; Pred. No. 0.17; Mismatches 25; Indels 25; Gaps 8;  
 Matches 43; Conservative 25; Mismatches 25; Indels 25; Gaps 8;

QY 600 LVLDVVC-----KPGESDFCLKVEAAVLGATGADPSQSHSGHGGDQDGEARPAL 651  
 Db 189 LGLDVCLSLRRRRRPPPTSPSRKQS---GASGHAEGRTDDEGGREEG--APAP 243  
 QY 652 DGSAAQLPLHTVKGSPDMRPGSDYDSSVP---SSLSPLMEGLSTDQETSSLTE 708  
 Db 244 PGARA-----GGGAGSPARTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 295  
 QY 709 SVSSSSGLG-EEPPALPSKLLSSGCKA 736  
 Db 296 AAQDPRGSGEOPSAAPSRLAAPSCSS 324

RESULT 14  
 Q96KN9 PRELIMINARY; PRT; 370 AA.  
 AC Q96KN9  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Connexin40.1.  
 GN CX40.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP Elberger J., Sehl G., Willocke K.;  
 RA "Structural and functional diversity of connexin genes in the mouse  
 and human genome";  
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF414564; CAC93846.1;  
 DR InterPro; IPR000500; Connexin.  
 DR Pfam; PF00029; connexin; 1.  
 DR PROSITE; PS00407; CONNEXINS\_1; UNKNOWN\_1.  
 DR PROSITE; PS00408; CONNEXINS\_2; UNKNOWN\_1.  
 SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 2.8%; Score 111.5; DB 4; Length 370;  
 Best Local Similarity 28.9%; Pred. No. 0.18;  
 Matches 43; Conservative 25; Mismatches 25; Indels 25; Gaps 8;

QY 600 LVLDVVC-----KPGESDFCLKVEAAVLGATGADPSQSHSGHGGDQDGEARPAL 651  
 Db 211 LGLDVCLSLRRRRRPPPTSPSRKQS---GASGHAEGRTDDEGGREEG--APAP 265  
 QY 652 DGSAAQLPLHTVKGSPDMRPGSDYDSSVP---SSLSPLMEGLSTDQETSSLTE 708  
 Db 266 PGARA-----GGGAGSPARTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 317  
 QY 709 SVSSSSGLG-EEPPALPSKLLSSGCKA 736  
 Db 318 AAQDPRGSGEOPSAAPSRLAAPSCSS 346

RESULT 15  
 Q9NTU6 PRELIMINARY; PRT; 428 AA.  
 AC Q9NTU6  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 45.4 kDa protein.  
 GN DKF2P434P21.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

(1)  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-TESTIS;  
 RC MEDLINE-21134917; PubMed-11230166;  
 RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ansgorge W., Boecker M., Bloecher H., Bauersachs S., Blum H.,  
 RA Leuber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,  
 RA Hewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Poustka A.;  
 RT "Towards a Catalog of Human Genes and Proteins: Sequencing and  
 Analysis of 500 Novel Complete Protein Coding Human CDNAS";  
 RL Genome Res. 11:422-435(2001).  
 DR EMBL; AL117401; CAB55902.2;  
 KW Hypothetical protein.  
 SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FDB3EE CRC64;

Query Match 2.7%; Score 110; DB 4; Length 428;  
 Best Local Similarity 23.5%; Pred. No. 0.31;  
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 474 KLRQAKOSS-SAALSKEFIAYFDYSCGDVPGI-----LDLSTKYLMDNLPQ 520  
 Db 103 RYNQTSQTSWTSCTNRNAISSYSTGGLPKRRRGPASSHCQLTLSSSKTYSRDPQ 162  
 QY 521 LGSLLHRSDHGLQEQ--PGQHTROGSRNRYFRSKGRSLYVAICNNHOFIDEEPDMFEKOF 578  
 Db 163 AVSSSGTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKF---PLLPRRG 210  
 QY 579 VPFH-PPPL-----RYREPVLKFDGSLVNDVM---CKPESDFCLKEAA 622  
 Db 211 EPLMLPPLELGYRVTVEDLDREKAAAFQINSAQVEDKAIQCRFSRSH---TLSSL 267  
 QY 623 VLGATG-PADQSHESQHGGLDQDGEARPALDGSAAQLPLHTVKGSPDM-----RD 675  
 Db 268 ATGASGLPAVSKAPS-----MDAQQETHKSDQCGLLDPLASA--AGVFTAPMSGKKHRP:321  
 QY 676 SG-IVDSVFPSSLSPLMEGLSTDQETSSLTESVSSSSGLGEEPPALPSKLLSSG 732  
 Db 322 PGPLFSSSDP-----LPATSSDSQDSQAQVTSLI-----PAPPPAASMDAG 361

Search completed: May 6, 2003, 13:44:47  
 Job time : 103 secs



GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: May 6, 2003, 13:41:56 ; Search time 30 Seconds  
(without alignments)  
738.515 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWALQSVFTNACING.....CKADLGRSTDELHVAFL 753

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

- 1: /cgn2.6/ptodata/1/iaa/5A-COMB.pep.\*
- 2: /cgn2.6/ptodata/1/iaa/5B-COMB.pep.\*
- 3: /cgn2.6/ptodata/1/iaa/5A-COMB.pep.\*
- 4: /cgn2.6/ptodata/1/iaa/5B-COMB.pep.\*
- 5: /cgn2.6/ptodata/1/iaa/PCTUS-COMB.pep.\*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	312	7.8	866	2	US-08-620-694A-10
2	312	7.8	866	3	US-09-022-255-10
3	312	7.8	866	3	US-09-022-696-10
4	312	7.8	866	3	US-08-978-773-4
5	312	7.8	866	3	US-09-022-253-10
6	312	7.8	866	3	US-09-022-260-10
7	312	7.8	866	4	US-09-022-259-10
8	312	7.8	866	4	US-09-022-257-10
9	306	7.6	864	2	US-08-620-694A-2
10	306	7.6	864	3	US-09-022-696-2
11	306	7.6	864	3	US-09-022-255-2
12	306	7.6	864	3	US-08-978-773-2
13	306	7.6	864	3	US-09-022-253-2
14	306	7.6	864	4	US-09-022-260-2
15	306	7.6	864	4	US-09-022-259-2
16	306	7.6	864	4	US-09-022-257-2
17	116.5	2.9	993	1	US-08-348-143-1
18	116.5	2.9	993	1	US-08-571-785-1
19	116.5	2.9	993	4	US-09-192-435-1
20	116.5	2.9	993	4	US-09-358-340-1
21	115	2.9	998	2	US-08-449-645A-20
22	115	2.9	998	2	US-08-702-367A-20
23	115	2.9	998	5	PCT-US95-04681-20
24	113.5	2.8	617	4	US-09-188-930-303
25	99	2.5	595	1	US-08-468-036-3
26	99	2.5	595	2	US-08-376-843-3
27	97	2.4	951	1	US-08-162-809-2

28	96	2.4	424	3	US-09-309-668-17	Sequence 17, Appl
29	96	2.4	424	5	PCT-US94-12933A-18	Sequence 18, Appl
30	96	2.4	984	2	US-08-673-785-6	Sequence 6, Appl
31	95	2.4	933	4	US-08-764-870-14	Sequence 14, Appl
32	95	2.4	933	4	US-08-980-115-14	Sequence 14, Appl
33	94	2.3	424	4	US-09-025-580-32	Sequence 32, Appl
34	94	2.3	3224	2	US-08-705-660-34	Sequence 34, Appl
35	94	2.3	3224	3	US-08-989-045-34	Sequence 21, Appl
36	93.5	2.3	828	2	US-08-993-228-21	Sequence 32, Appl
37	92.5	2.3	347	4	US-08-630-915A-32	Sequence 1, Appl
38	92.5	2.3	2308	1	US-08-015-973-1	Sequence 1, Appl
39	92.5	2.3	2308	2	US-08-448-164-1	Sequence 2, Appl
40	92.5	2.3	2308	4	US-08-081-929-2	Sequence 2, Appl
41	92.5	2.3	2314	4	US-09-816-703A-2	Sequence 2, Appl
42	91.5	2.3	1838	4	US-09-120-663-2	Sequence 12, Appl
43	90.5	2.3	483	2	US-08-583-562B-12	Sequence 12, Appl
44	90.5	2.3	483	2	US-08-779-113-12	Sequence 2, Appl
45	90.5	2.3	857	2	US-08-779-113-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-620-694A-10  
Sequence 10, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-620-694A-10

Query Match

7.8% Score 312; DB 2; Length 866;

Best Local Similarity 23.18; pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTLNPKVGRVIADAQNI-----ISOYACHDQ-----VAVTILMS 113  
Db 49 NCTVKNSTCLDSWIHP-----RNLTPSSPKDLQIQLHFAHQOQDLFPVAHLEWT 99

QY 114 -PGALGIEFLKGRVILELSEKROCOQIILKDPKQNSFKRTCHESQPLNKKFTD 172  
Db 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTSHFV--VDPOE 156

QY 173 YFVKV--VPPFSIKNESYHFFFTTRACDLLOPDNLACK-----PFWKPRNL-----219  
Db 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPCDEHARKVTTTCKMS96SDWP--NTTVETLEAH 215

QY 220 -----NISQSGSDMOVSFOHAPNFGPRFFYLHYLKLHKGPKKRTCKOQTETT 270  
Db 216 QLRVSTFLNETHYQILLTSFPHNENHSCFEHMH--HIPAPRPEEPHORSNVTLRNLK 274

QY 271 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPNAGPIRAVAITVPLVVISAF 327  
Db 275 GCCHQVQIQPFSSCLNDCLRHSAVSCPEMDTPEIPDYNEPLWYFTGIGISILLVG 334

QY 328 ATLTVMCRKROENIYSHLDESSSTYTAALPRERLRPR-----KVFCLYSSKQGN 383  
Db 335 SVILLIVCHTNRLAGPGS---EKSDTKYTDGLPAADLIPPLKPKRWIIYSA--DHPL 390

QY 384 HMYVQCFAFYFLQDPCGCEVALDWDLSLCREGQEWY----IQKHESQFIIVVCSKG 439  
Db 391 YVDVWLKFAOFLLTACGTEVALDLEEQAISEAGVMTWVGRQKQEVESNRIIVLCRSG 450

QY 440 MRYEVDKKNYKHGGG-----RSGSGELFLVAVSAIAEKLQAKOSSAALSKEIFA 491  
Db 451 TR-----AKQALLGAGPVRLCDHGKPVGDLTAAAMNLLPDKR-----PACGTVTV 501

QY 492 VYF--DYSCBQDVPGLDILSTKYRLMDNLQCLSHLSRHDGLQEPQHTROG--SRNRYF 548  
Db 502 CYFEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559

QY 549 RSKGRSLYVAICNNHOFIDEEPDMFE-----KQVYFPHPPPLRYRVEKFDGSL 600  
Db 560 RSPGROLRAALDRFDMQVRCDFWFCENLYSADDQAPSLDEEV--FEPLDPP--GTGI 617

QY 601 VLDNVCKPSPSDCLKVEAYVIGATGPADSOHE-----SQHGG 640  
Db 618 VKRAPLVRE--PGSOACLAIDPLVGEEGAVALKLEPHIQPRQOPAPQPLTLVLAEEGA 676

QY 641 LDODGEARPALDGA---ALQ-----PLHTVYKAGSPDMRDSGIYDSSVPSSELSLP 691  
Db 677 LVAAVEGRLADGAVALALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727

QY 692 LMEGSLTDQETSSITESVSSSGLGEEPPALPSKLLSSGSKRADLGC 740  
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEOISLSCQAQGC 768

RESULT 2  
US-09-022-255-10  
Sequence 10, Application US/0902255  
Patent No. 6072033  
GENERAL INFORMATION:  
APPLICANT: Yeo, zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-255-10

Query Match 7.88; Score 312; Db 3; Length 866;  
Best Local Similarity 23.18; Pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTLNPKVGRVIADAQNI-----ISOYACHDQ-----VAVTILMS 113  
Db 49 NCTVKNSTCLDSWIHP-----RNLTPSSPKDLQIQLHFAHQOQDLFPVAHLEWT 99

QY 114 -PGALGIEFLKGRVILELSEKROCOQIILKDPKQNSFKRTCHESQPLNKKFTD 172  
Db 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTSHFV--VDPOE 156

QY 173 YFVKV--VPPFSIKNESYHFFFTTRACDLLOPDNLACK-----PFWKPRNL-----219  
Db 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPCDEHARKVTTTCKMS96SDWP--NTTVETLEAH 215

QY 220 -----NISQSGSDMOVSFOHAPNFGPRFFYLHYLKLHKGPKKRTCKOQTETT 270  
Db 216 QLRVSTFLNETHYQILLTSFPHNENHSCFEHMH--HIPAPRPEEPHORSNVTLRNLK 274

QY 271 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPNAGPIRAVAITVPLVVISAF 327  
Db 275 GCCHQVQIQPFSSCLNDCLRHSAVSCPEMDTPEIPDYNEPLWYFTGIGISILLVG 334

QY 328 ATLTVMCRKROENIYSHLDESSSTYTAALPRERLRPR-----KVFCLYSSKQGN 383  
Db 335 SVILLIVCHTNRLAGPGS---EKSDTKYTDGLPAADLIPPLKPKRWIIYSA--DHPL 390

QY 384 HMYVQCFAFYFLQDPCGCEVALDWDLSLCREGQEWY----IQKHESQFIIVVCSKG 439  
Db 391 YVDVWLKFAOFLLTACGTEVALDLEEQAISEAGVMTWVGRQKQEVESNRIIVLCRSG 450

QY 440 MRYEVDKKNYKHGGG-----RSGSGELFLVAVSAIAEKLQAKOSSAALSKEIFA 491  
Db 451 TR-----AKQALLGAGPVRLCDHGKPVGDLTAAAMNLLPDKR-----PACGTVTV 501

QY 492 VYF--DYSCBQDVPGLDILSTKYRLMDNLQCLSHLSRHDGLQEPQHTROG--SRNRYF 548  
Db 502 CYFEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559

QY 549 RSKGRSLYVAICNNHOFIDEEPDMFE-----KQVYFPHPPPLRYRVEKFDGSL 600



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Db 560 RSPGRLRALDRFDMQVRCDFECENLYSADDDQAPSLDEEV-FEELPLP-GTGI 617
QY 601 VLNDVCKPGPESDFCLKVAIVLGAATGADSGHE-----SOHGG 640
Db 618 VKRAPLVRE-FCGQACLAIDPLVGEEGAANKLEPHLQPGQAPQLHTLVLAEEGA 676
QY 641 LDQDGEARALDGA---ALQ-----PLLHTVKAGSPDMPSGIYDSSVPSSELSLP 691
Db 677 LVAAVEPGPLADGAANRLALAGEACPLLAGSPGAG-----RNSVLE---LPVDPEDSP 727
QY 692 LMGLSTDOTETSSLTSSVSSSGLEGEPEPALPSKLLSGSGCKADLGC 740
Db 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

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## RESULT 3

```

US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037

```

## GENERAL INFORMATION:

```

; APPLICANT: tao, zhenblin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

```

## COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.696

```

## FILING DATE:

```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620.694

```

## CLASSIFICATION:

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410.535
; FILING DATE: 23 MARCH 1995

```

## ATTORNEY/AGENT INFORMATION:

```

; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,995
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

```

## INFORMATION FOR SEQ ID NO: 10:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-696-10

```

```

Query Match 7.8%; Score 312; DB 3; Length 866;

```

```

Best Local Similarity 23.1%; Pred. No. 1.9e-23;

```

```

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

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```

QY 69 NITFKYDNC--TTLNPNVGRHVIADAQNT-----ISOYACHQ-----VAATILMS 113

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Db 49 NCTVKNSTCLDSDSIHP-----RNLTPSPKDLQIQLHFHTQGDLPFAHLEWT 99

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QY 114 -PGALGIFLEGFRVILEELKSEGRCCOOLILKQPLKASSFKRTGMSQFLNNAFETD 172
Db 100 LOTDASILYLGSAELSVIQLNTERLCVR--FEFLSKLHHRRWRFTTSFEV-VDPDR 156
QY 173 YFVKV--VPFISIKENSYHFFFRTRACDLLOPONLACK---PFWKPRKL----- 219
Db 157 YEYVTHLFPKIPDGNPHOSKNFLVPCDEHARKVVTTCMSSGSLMDP-NITVETLEAH 215
QY 220 -----NLSQSGDMQVSDHAPHNFGFRFFYLHYKLHKGEGFKKTKCKQBTET 270
Db 216 QLRVSFTLWNESTHYQLITSPPHNEHSCFEHMH-HIPAPRPEEFHQRSNVTILNLK 274
QY 271 SCLQNVSPGDIYILELVDYT--NTRKVMYALKPVHSPWAGPIRAVAITVPLWISAF 327
Db 275 GCRHOYQIQPFSSCLNDLRSATVSCPEMDTPEPIDYMLPLWVYFETIGSILLVG 334
QY 328 -ATLFTVMCKKQOENIYSHLDESSSESTYTAALPRELEPRP-----KVELCTSSKDGQ 383
Db 335 SVILLIVCTWRLAGPGS---EKISDRTYDGLPAADLIPPLAPRKVWYIISR-DHPL 390
QY 384 HNVVOCFAIFLQDFGCEVALDMDWFSLCRSGREWY----IOKHESOFIIVVCSKG 439
Db 391 YVDWLKPAQLLTACGTEVALDLLEQAISEAGVMTWVGROKQEMVESNKIIVLCRSG 450
QY 440 -MYFVDKNTYKHGGG-----RSGKGELFLVAVSAIAEKLRQAKQSSSAALSFKTA 491
Db 451 -TR-----AKWOALLGRGAPVRLCRDHGKPVGLFTAAAMNMLPDFKR-----PACFGTYV 501
QY 492 VYF-DYSCGIDVPGILDSTKYLMNLPLQCLSHLSRDHGLQEPQHTROG--SRRTYF 548
Db 502 CYFSEVSCDGVDPDFCAAPRYPLADREFEV--YFRIQDLEMFQGRMHRVGLSGDNL 559
QY 549 RSKGRSLYVAICNMHGFIDEEPWFPE-----KQFVPPHPPPLRYREPVLEKFDGSL 600
Db 560 RSPGRLRALDRFDMQVRCDFECENLYSADDDQAPSLDEEV-FEELPLP-GTGI 617
QY 601 VLNDVCKPGPESDFCLKVAIVLGAATGADSGHE-----SOHGG 640
Db 618 VKRAPLVRE-FCGQACLAIDPLVGEEGAANKLEPHLQPGQAPQLHTLVLAEEGA 676
QY 641 LDQDGEARALDGA---ALQ-----PLLHTVKAGSPDMPSGIYDSSVPSSELSLP 691
Db 677 LVAAVEPGPLADGAANRLALAGEACPLLAGSPGAG-----RNSVLE---LPVDPEDSP 727
QY 692 LMGLSTDOTETSSLTSSVSSSGLEGEPEPALPSKLLSGSGCKADLGC 740
Db 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

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## RESULT 4

```

US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906

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## GENERAL INFORMATION:

```

; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

```

## COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978.773
; FILING DATE:
; CLASSIFICATION: 530

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2623-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-773-4

Query Match 7.8%; Score 312; DB 3; Length 866;  
Best Local Similarity 23.1%; Pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TYTLPVGVKVIADAQNT-----ISQYACHDQ-----VAVTILWS 113  
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSPKDLQIQLHFAHTQOQDLFPVAHIEWT 99  
QY 114 -PGALGTEFLKGRVLEELSEKSGROCOQLIKDPKOLNSFKRTGMSQPELNKKPFTD 172  
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRHWRFTSHEV-VDPDQE 156  
QY 173 YFVKV--VFPSPKSNESYHFFFTTRACDILLQPDNLAK-----PFWKPRNL----- 219  
DB 157 YEVTVHLPKPIPDGDPNHSKNFLVPDCEHARKMVTTPCMSSGSLMDP-NITVETLEAH 215  
QY 220 -----NISQHSQDMQVSDHAPNFGFFRYFLHYKLGHEGPKFKTKCQQTETT 270  
DB 216 QLRVSTLWNSTHYQILLTSFPMENHSCFHHM-HIPAPRPEEFHQRKSVTLTLNLK 274  
QY 69 NITFKYDNC--TYTLPVGVKVIADAQNT-----ISQYACHDQ-----VAVTILWS 113  
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSPKDLQIQLHFAHTQOQDLFPVAHIEWT 99  
QY 114 -PGALGTEFLKGRVLEELSEKSGROCOQLIKDPKOLNSFKRTGMSQPELNKKPFTD 172  
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRHWRFTSHEV-VDPDQE 156  
QY 173 YFVKV--VFPSPKSNESYHFFFTTRACDILLQPDNLAK-----PFWKPRNL----- 219  
DB 157 YEVTVHLPKPIPDGDPNHSKNFLVPDCEHARKMVTTPCMSSGSLMDP-NITVETLEAH 215  
QY 220 -----NISQHSQDMQVSDHAPNFGFFRYFLHYKLGHEGPKFKTKCQQTETT 270  
DB 216 QLRVSTLWNSTHYQILLTSFPMENHSCFHHM-HIPAPRPEEFHQRKSVTLTLNLK 274

Db 728/L--GSSTPMASDILPEDVR-----EHLGGLMLSLPSILSCAOAGGC 768  
RESULT 5  
US-09-022-253-10  
Sequence 10; Application US/09022253  
Patent No: 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-253-10

Query Match 7.8%; Score 312; DB 3; Length 866;  
Best Local Similarity 23.1%; Pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TYTLPVGVKVIADAQNT-----ISQYACHDQ-----VAVTILWS 113  
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSPKDLQIQLHFAHTQOQDLFPVAHIEWT 99  
QY 114 -PGALGTEFLKGRVLEELSEKSGROCOQLIKDPKOLNSFKRTGMSQPELNKKPFTD 172  
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRHWRFTSHEV-VDPDQE 156  
QY 173 YFVKV--VFPSPKSNESYHFFFTTRACDILLQPDNLAK-----PFWKPRNL----- 219  
DB 157 YEVTVHLPKPIPDGDPNHSKNFLVPDCEHARKMVTTPCMSSGSLMDP-NITVETLEAH 215  
QY 220 -----NISQHSQDMQVSDHAPNFGFFRYFLHYKLGHEGPKFKTKCQQTETT 270  
DB 216 QLRVSTLWNSTHYQILLTSFPMENHSCFHHM-HIPAPRPEEFHQRKSVTLTLNLK 274

QY 271 SCILQNVSGDYIIIEVDVT---NTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 327  
 DB 275 GCRHQVQIQPFSSCLNCLHSATVSCPEMPTPEPIIDYMLPMVWTFITGISILLVG 334  
 QY 328 ATFTVCKRKKOENIYSHLDESSSTYTAALPRERLRPR---KVFICYSKDKQN 383  
 DB 335 SVILLVCMTNLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPKVWIIYSA-DHPL 390  
 QY 384 HMVVOCFAYFLQDCGEVALDMEFSLCREGOREW---IQKIHESOFIIVVCSKG 439  
 DB 391 YVDVVLKFAQFLITACGTEVALDLEEQALISEAGVWTVGKQKQWESNKIIVLCRG 450  
 QY 440 MKYFDKKNYKHGGG---RSGKGEFLVAVSAIAEKLRQAKSSAALSFA 491  
 DB 451 TR---AKWQALLRGAPVRLCDHGKPVGDLFTAAAMNMLPDFKR---PACFGYVV 501  
 QY 492 VYF-DYSCGDPVGLDSTKYRLMDNLPOLCSHLHSDRGLOEPCQHTROG---SRNRYF 548  
 DB 502 CYSEVSCDGVDPDLFGAPRYPLADRFEEV---YFRIQDLEMFGPGRHVRVGLSGDNL 559  
 QY 549 RSKSGRLVYACNMHOFIDEEPWFEE---KQVFPHPPLRYREPVLKFDGSL 600  
 DB 560 RSPGGRQLRAALDRFRDMQVRCDFWECENLYSADQDAPSLDEEV-FEELPLPP-GTGI 617  
 QY 601 VLNDVCKPGSPDCLKVEAAVLGATGPADSQHE---SOHGG 640  
 DB 618 VKRAPLVRE-PSQACLAIDPLVGEEGAARVAKLEPHLQPRGQAPQPLHTLVLAEEGA 676  
 QY 641 LDODGEARALDGS---ALQ---PLHTVTKAGSPDMPSDIYDSSVPSSLSLP 691  
 DB 677 LYAAVEPGPLADGAARVLAAGEACPLLAGPCAG---RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGLSDTQDTETSSITSVSSSGLEGEPPALPSKLLSGSCADLGC 740  
 DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

## RESULT 6

US-09-022-260-10  
 ; Sequence 10, Application US/09022260  
 ; Patent No. 6100235

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, Melanie  
 APPLICANT: Fanelow, William  
 TITLE OF INVENTION: No. 6100235el receptor That Blinds IL-17  
 NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

ADDRESSES: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA

ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,260

## FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

## FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 866 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-260-10

Query Match 7.88; Score 312; DB 3; Length 866;

Best Local Similarity 23.18; Pred. No. 1.9e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TLYLNPVGVKHVIADAQNIIT-----ISOYACHDQ-----VAVTILMS 113

DB 49 NCTVKNSTCLDSDSIHP-----RNLTPSPKDLQQLHPAHTQOQGLFPVAHIEMT 99

QY 114 PCALGIEFLAGFRVILEELKSEGRQOOLIKDKPKOLNSSFARTGMESQPLNKKFETD 172

DB 100 LQTDASILYLEGAEISVLQNTNERLCVR--FEELSKLRHHHRWRFTFSHEV-VPDQZ 156

QY 173 YFVKV--VPEFSIKNESNYHPFFETRACDILLQPDNLACK---PFWKPRNL----- 219

DB 157 YEYVHHLPKPIPOCDNDHOSNLFVDPCEHARMKVTPCMSSGSLADP-NITVETLEAH 215

QY 220 -----NISQSGSDQVSDHAPHNGFRFFLYHKLKHEGPKFKTKCQQTTEYT 270

DB 216 QLVSTFWLNSTHYQILLTSFPHNHNSCFEHRH-HIPAPRPEFHORSNVTJTLRNKL 274

QY 271 SCILQNVSGDYIIIEVDVT---NTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 327

DB 275 GCRHQVQIQPFSSCLNCLHSATVSCPEMPTPEPIIDYMLPMVWTFITGISILLVG 334

QY 328 ATFTVCKRKKOENIYSHLDESSSTYTAALPRERLRPR---KVFICYSKDKQN 383

DB 335 SVILLVCMTNLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPKVWIIYSA-DHPL 390

QY 384 HMVVOCFAYFLQDCGEVALDMEFSLCREGOREW---IQKIHESOFIIVVCSKG 439

DB 391 YVDVVLKFAQFLITACGTEVALDLEEQALISEAGVWTVGKQKQWESNKIIVLCRG 450

QY 440 MKYFDKKNYKHGGG---RSGKGEFLVAVSAIAEKLRQAKSSAALSFA 491

DB 451 TR---AKWQALLRGAPVRLCDHGKPVGDLFTAAAMNMLPDFKR---PACFGYVV 501

QY 492 VYF-DYSCGDPVGLDSTKYRLMDNLPOLCSHLHSDRGLOEPCQHTROG---SRNRYF 548

DB 502 CYSEVSCDGVDPDLFGAPRYPLADRFEEV---YFRIQDLEMFGPGRHVRVGLSGDNL 559

QY 549 RSKSGRLVYACNMHOFIDEEPWFEE---KQVFPHPPLRYREPVLKFDGSL 600

DB 560 RSPGGRQLRAALDRFRDMQVRCDFWECENLYSADQDAPSLDEEV-FEELPLPP-GTGI 617

QY 601 VLNDVCKPGSPDCLKVEAAVLGATGPADSQHE---SOHGG 640

DB 618 VKRAPLVRE-PSQACLAIDPLVGEEGAARVAKLEPHLQPRGQAPQPLHTLVLAEEGA 676

QY 641 LDODGEARALDGS---ALQ---PLHTVTKAGSPDMPSDIYDSSVPSSLSLP 691

DB 677 LYAAVEPGPLADGAARVLAAGEACPLLAGPCAG---RNSVLF---LPVDPEDSP 727

QY 692 LMEGLSDTQDTETSSITSVSSSGLEGEPPALPSKLLSGSCADLGC 740

DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

## RESULT 7

US-09-022-259-10

Sequence 10, Application US/09022259

Patent No. 6191104

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,259

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 866 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-259-10

Query Match 7.8%; Score 312; DB 4; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.9e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITKYNDC---TYLNPVKHVIADAQNT-----ISYACHDQ-----VAVTILWS 113  
 DB 49 NCTVNSTCLDDSWIP-----RLTPSPKDLQIQLEFAHTQGGDLFPVAHIEWT 99  
 QY 114 -PGALGTEFLKGRVILEELKSGGCOQLILKDPKQNSFKRTGMESOPFLNKKFTED 172  
 DB 100 LQTDASILYLEGAELSVLQATNTERLCVR--FEFLSKLHHHRWRFTSFHFV-VDPQEE 156  
 QY 173 YFVKY--VPFFSKNSYHFFFTFRACDILLQPDNLACK---PFWKPRNL----- 219  
 DB 157 YEVTVHLPKPIPGDPNHSKNFLVPDCEHAKMVTTPCKSSGSLMDP-NITVTELEAH 215  
 QY 220 -----NISQSGDMQVSDPHAFNFCFFFLYHLKHEGPKKTKCKEQQTETT 270  
 DB 216 QLRVSTFLWNESTHYOILLTFFHNEHSCFEHMH-HPAPRPEPHQRNVTLLRLMK 274  
 QY 271 SCLQNVSPGDIYELVDOT-----NTRKVMHYALKPVSPWAGPIRAVATVPLVVISAF 327  
 DB 275 GCRHQVOIQFSSCLNDCLRHSAVSCPEMDTPEPIQYPMPLWYWEITGISLLVG 334  
 QY 328 ATLFTVMCRKQKQENTYSHLDESSESSTYTAALPRRLRPRP-----KVFCLYSSKDSQN 383

DB 335 SVILLIVCMTRLRAGPS---EKYSDDTKYTDGLPADLTPPLPKPKVKYIIISA-DHPL 390  
 QY 384 HNNVQCFAFELQDFCGCEVALDIMEFSLCREGQREKV---LOKHESQELIVVCSKG 439  
 DB 331 YDVVLEKFAQFLITACGTEVALDILEEQAISAGVYVWVGKQKQKQKQKQKQKQKQKQ 450  
 QY 440 KMYEVKDKNNKHKGG-----RSGGKGLFLVAVSAIAEKLRQAKQKSSAALSUFIA 491  
 DB 451 TR-----AKWQALIGRGAAPVRLRCHGKPGVDLFTAMNMILPDKR-----PACFTYV 501  
 QY 492 YTF-DYSCBQVPGILDLSTRYLMONLPQALSHLSRQGLQEPQCHTRQO---SRNRYF 548  
 DB 502 CYFSEVSCDQVDFLGAAPRYPLMDRFEV--YFRIQDLEMPQPGMRHVRVGLSGNYL 559  
 QY 549 RSKGRSLYVAICNMHOFIDEEPWF-----KQFVPEPPEPPEPPEPPEPPEPPEPPE 600  
 DB 560 RSPGGRGLRAALDRFRDMQVRCPECEENLYSADDQADAFSLDEEV-FPEELPP-GTGI 617  
 QY 601 VLNDVCKKCPESDFCLAVEAVALGATGADSOHE-----SCHGG 640  
 DB 618 VKRAPLVRE-PSQACLAIDLVEGEGGAVALKLEPHLOPRGQAPQPLTLVLAEEGA 676  
 QY 641 LDQGEARPALDGS---ALQ-----PLHVVKAGSPDMPDPSGIYSSVPSSELSLP 691  
 DB 677 LVAAVEPGLADGAARLALAGEAGEACPLLGSPGAG-----RNSVLF---LPVDPDPS 727  
 QY 692 LMEGLSTDQDETSSILTESVSSSGIAGEEPPALPKSLSSGSCCKADLGC 740  
 DB 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSQAOAGGC 768

# RESULT 8

US-09-022-257-10

Sequence 10, Application US/09022257

Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,257

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 866 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 OS-09-022-257-10

Query Match 7.88; Score 312; DB 4; Length 866;  
 Best Local Similarity 23.18; Pred. No. 1.9e-23;  
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTLNPKVGRHVIADQNI-----ISOYACHDQ-----VAVTLWS 113  
 DB 49 NCTVKNSCLDSDWHP-----RNLTPSSPKDQLQHPAHTQGGDLFPVAHEWT 99  
 QY 114--PCALGIEPLGKGRVILEELKSGROCOQLILKOPKOLNSFKFKGMSQPFLLKKEFTD 172  
 DB 100 LQTDASILYLEGAEISVLQNLNHERLCVR--FEFLSKLRHHRRRTFSHEV-VDPDQE 156  
 QY 173 YFKVY--VDFPSIKNESNYPPFFTRACDILLQDMLACK---PFWKPRNL-----219  
 DB 157 IEVTVHLLPKPIPDGDPNHQSKNLFVPCCEHARKMVTTPCMSSGSLMDP-NITVETLEAH 215  
 QY 220 -----NISQSGDMQVSYDFHAPNHFGRFFYLHYKLKHEGPFKRTCKQQTETT 270  
 DB 216 QLRVSTFLWNSTHYQILLTSFPHMNSCFEHHM-HIPAPRPEFHQRSNVTTLNLK 274  
 QY 271 SCILQWSPGVYIELVDYD-----NTRKVMYALKPVHSPWAGPIRAVAITVPLVISAF 327  
 DB 275 GCRHQVQIOPFSSCLNDCLRESATVSCPMPDTPPIPYMPLVWYFVITGSIILVG 334  
 QY 328 ATLTVMCRKKQENIYSHLDESSSESYTAALPRERLRPP-----KVFLCYSSKQCN 383  
 DB 335 SVILLVCMYRLAGRS---EYSDTKYDGLPAADLIPPLPRKVIITISA-DHPL 390  
 QY 384 HMYVOCRAYFLDPGCECEVALDIEDFSLCRQREW-----IOKHESOFILVCSKG 439  
 DB 391 IYDVILKACPLTACTEVALDIEQAISEGVTWGRQKQEMVESNKIIVLCRSRG 450  
 QY 440 MYTFVKKNYKHGG-----RSGKGELFLVAVSAIAEKLQKQAKOSSAALSFKIA 491  
 DB 451 TR-----AKWQALLGKAPVRLCDHGKPVGDLFTAAANNMLPDFR-----PACFGTYV 501  
 QY 492 VYF-DYSCGVDPGILDLSTKYRLADNLPOLCSHLHSRDHGLQEPGQHTROG---SRRTYF 548  
 DB 502 CYSEVSCDGVDPOLGAAPRYPLMDRFEV--YFRIODLEMFQGRHVRVGLSGDNYL 559  
 QY 549 RSGSGSLYVAICNWHOFIDEEDWFE-----KQFVPEHPPLRYRPEVLEKFSGL 600  
 DB 560 RSPGRLAALDRFQWVRCDFEFCENLYSADQDAPSLDEEV-FEPLLP-GTGI-617  
 QY 601 VLDVWCKPSPESDFCLKEAVLGAATGAPDSQHE-----SOHGG 640  
 DB 618 VKRAPLVRE-PGSOACLAIDPLVBEGBGAAYAKLEPHLOPQCPAPQLHTVLVAEBA 676  
 QY 641 LQDGEARPALDGA---ALQ-----ELLHTYKAGSPDMRDSGIYDSSVPSSELSLP 691  
 DB 677 LVAAVEPGPLADGAVALALAGEACPLGSPGAG-----RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGLSTQDTSTSLTESVSSSGLGEERPPALPSKLLSGSKADLGC 740  
 DB 728 L--GSSTPMASPOLLPDYR-----EHLGLMLSLFEQSLSCQAQGC-768

## RESULT 9

US-08-620-694A-2  
 Sequence 2, Application US/08620694A  
 Patent No. 5869286  
 GENERAL INFORMATION:  
 APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 5869286el Receptor That Blinds IL-17

NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER-READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/620,694A  
 FILING DATE: 21 MARCH 1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/538,765  
 FILING DATE: 7 AUGUST 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-620-694A-2

Query Match 7.68; Score 306; DB 2; Length 864;  
 Best Local Similarity 22.58; Pred. No. 8.2e-23;

Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GNRM-----KAAARPL-----CVANEGVGPSNRSLNITFKYDNCITLNPVK 86  
 DB 17 GWLLLLNVLAPGRASPRLLDPAPVCAQESLSCVKNSTCIDDSWIHPNLTTPSSPKNI 76  
 QY 87 HVIADAQNIITISQFACHQVAT--ILNS--PGALGIEPLGKGRVILEELKSGROCOQ---141  
 DB 77 YI-----NLSVSTQHGLVPPVLYHVETLQTDASILYLEGAEISVLQNLNHERLCVKPQ 131  
 QY 142 --LILKDKPOLNSFRTGMSQPFLLKKEFTDYFKVVPFSPKINSESNYHPFFETTRAC 199  
 DB 132 LSKLQHKKRRFS-----SHEVVDPGQYEVTVHHLKPKIPDGDPNHKSILFVPC 185  
 QY 200 D-----LLQLPDNLACKPFWKPRNLNI-----SOH-----GSDMQV 230  
 DB 186 EDSKMKTTSCVSSGSLMDP-NITVETLDTQHLRVDFTLWNSTPYVLLSESDSENHS 244  
 QY 231 SFD-----HAPNFGPRFFYLHYKLKHE---GPKRTCKQEQTTETTSCLL 274  
 DB 245 CDFVYKQIFAPROEEFHQRANTFTLSKPFHCCCHHVQVQPF-FSSCLND-----CLR 296  
 QY 275 QNVSPGDYIIELVDDNTTKVMHYALKPV--HSP-WA-GPIRAVAITVPLVISAFATL 330  
 DB 297 HAVTVPCPVI-----SNMT-----VPKPVADYIPLWYGLITLIAL-----LLVGSVIL 341  
 QY 331 FVVMCRKQENIYSHLDESSSESYTAALPRERLRPRKPVFLCYSSKQGNHNVVQC 390  
 DB 342 IICMTWRLSGADQEKHGDDSKINGILPVDLTPEPLRPR-KVMIVISA-DRLPYVEVVLK 399  
 QY 391 FAYELQDFCCCEVALDIEDFSLCRQRENVOK-----IHESQFIIVCSKCKKIFYDK 446

Db 400 FAOPLITACCTEVALDLEBOVISEVGVMTWVSRQKOBMESKIIILCSRG-----TQ 454  
 QY 447 KNYKHGG-----GRSGKGLFVAVSAIAEKLQAKQSSSAKSLFAVFDY 496  
 Db 455 AKWKAILGNAEPVQLCRDHWKPGADLFTAAANNILPDFR-----PACFTYVYVCSG 509  
 QY 497 SC-EGDVPGLDSTKYRLMDNLPOLCSHLSDRGLOEPGQ--HTRQGSRRNFRSKG 553  
 Db 510 ICSERDVPDLFNITSRYPLADREEV--YFRIOLEMFEPGRHWHVRLTGMVLSQSPG 567  
 QY 554 RSLVVAICNMHOFIDEEPDMFEKOFVPHF-----PPLR---YREPYLEKFGSLVLDVM 606  
 Db 568 RQLKAVLRFQEMOTQCPDMFERENICLADGDLPSLDEEVFEDPLPP--GGIVKQOPL 626  
 QY 607 CKPGPESDCLKVEANVLGATGPADSOHESQHGGLDQ-----GEAR 648  
 Db 627 VREL-P--SDGCLVDDCV-----SEESRMALDQPLMPQRELVAHTLQSMVLPABQV 677  
 QY 649 PALDGSAAQLPILHTVKAQSPDMF--RDS-----GIYDSSV--PSELSLPL----- 692  
 Db 678 PA---AHVVEPLHLFDGSGAAQLPMTEDSEACPLLGVRNSILCLPVDSDPLCSTPM 734  
 QY 693 -----NEGSLDQDETETSLTESVSSSGGEEPPALPSPKLSGSCADLCGRSYTDE 746  
 Db 735 MSPDHLQGDAREQLSMLSVLQOISLQOPLESNPR-PEVVL-----GCTPSEEE 784

## RESULT 10

US-09-022-255-2

Sequence 2, Application US/09022255

Patent No. 6072033

## GENERAL INFORMATION:

APPLICANT: YAO, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,255

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/620,694

FILING DATE: 21 MARCH 1996

APPLICATION NUMBER: USN 08/538,765

FILING DATE: 7 AUGUST 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/410,535

FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

Query Match: 7.68, Score: 306, DB 3, Length: 864  
 Best Local Similarity: 22.98, Pred. No. 8.2e-23  
 Molecule Type: protein  
 US-09-022-255-2  
 Matches: 189; Conservative: 128; Mismatches: 319; Indels: 203; Gaps: 43;

QY 40 GWRM-----KAAARPL-----CVANEGVGPASRNSCLNITFKYONCTTLYNPNVGR 86  
 Db 17 GWILLANLAVPGASPRLLDPPAPVCAQEGSLCRVKNSTCLDSDNIHPPKMLPSSPKNI 76  
 QY 87 HVIADQNIITISQACHDOVAVT--ILWS--PGALGIEFLKGRVILBEELKSGRCQQ----- 141  
 Db 77 YI-----NLSVSSYQHGELVPVLRVETILQTDASILYLEGAELSLQNLNRLCVKFOF 131  
 QY 142 --LILADPKQLMSGFKRTGMSQPFLLKKFTDFVKKVFPFSLKSNESNYHFFFRTRAC 199  
 Db 132 LSLMLQHRRKRRFSF-----SHFVVDQGEVETVHHLKPIPDGDPNKKSKIIIFVDC 185  
 QY 200 D---LILQPDNLACKPPKPRNLNI---SQR-----GSDMQV 230  
 Db 186 EDSKMKMTTSCVSSGSLWDP--NITVETLTQHLAVDTLANESTPYOVLLSESDSENHS 244  
 QY 231 SFD-----HAPNFGFRFFYLHKLHE---GPFKRYCKQEOETTTSCLL 274  
 Db 245 CFQVVKQIFAPRQEEFORANVTFTLSKFHMCCHHVQVOFF--FSSCLND-----CLR 296  
 QY 275 QNVSPGDYIIELVDDTNTTRKVMYALAPV--HSP--WA--OPTIRAVAITVPLVVISAFATL 330  
 Db 297 HAVTVPCPVI-----SNT-----VPRPVADYIPLWVYGLITLAI-----LLVGSVIVL 341  
 QY 331 FTVMCKKKOENIYSHLDESSSSTYTAALPRERLRPRKPVLCVSKKQGNMNVVQC 390  
 Db 342 IICMTWRLSGADQEKHGDSKINGILPVADLTTPPLRPR--KWIIVYSA--DHPLIVEVVLK 399  
 QY 391 FAYFLODQCGCEVALDLEDFSLCRQGEWVIOK-----IHESQFLIVCSKGMKIFVDK 446  
 Db 400 FQGLITACGTEVALDLLEQVISEGVVMTWVSRQKOBMESKIIILCSRG-----TQ 454  
 QY 447 KNYKHGG-----GRSGKGLFVAVSAIAEKLQAKQSSSAKSLFAVFDY 496  
 Db 455 AKWKAILGNAEPVQLCRDHWKPGADLFTAAANNILPDFR-----PACFTYVYVCSG 509  
 QY 497 SC-EGDVPGLDSTKYRLMDNLPOLCSHLSDRGLOEPGQ--HTRQGSRRNFRSKG 553  
 Db 510 ICSERDVPDLFNITSRYPLADREEV--YFRIOLEMFEPGRHWHVRLTGMVLSQSPG 567  
 QY 554 RSLVVAICNMHOFIDEEPDMFEKOFVPHF-----PPLR---YREPYLEKFGSLVLDVM 606  
 Db 568 RQLKAVLRFQEMOTQCPDMFERENICLADGDLPSLDEEVFEDPLPP--GGIVKQOPL 626  
 QY 607 CKPGPESDCLKVEANVLGATGPADSOHESQHGGLDQ-----GEAR 648  
 Db 627 VREL-P--SDGCLVDDCV-----SEESRMALDQPLMPQRELVAHTLQSMVLPABQV 677  
 QY 649 PALDGSAAQLPILHTVKAQSPDMF--RDS-----GIYDSSV--PSELSLPL----- 692  
 Db 678 PA---AHVVEPLHLFDGSGAAQLPMTEDSEACPLLGVRNSILCLPVDSDPLCSTPM 734  
 QY 693 -----NEGSLDQDETETSLTESVSSSGGEEPPALPSPKLSGSCADLCGRSYTDE 746  
 Db 735 MSPDHLQGDAREQLSMLSVLQOISLQOPLESNPR-PEVVL-----GCTPSEEE 784

## RESULT 11

US-09-022-696-2

Sequence 2, Application US/09022696

Patent No. 6072037

## GENERAL INFORMATION:

APPLICANT: YAO, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,696  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-696-2

Query Match 7.6%; Score 306; DB 3; Length 864;  
Best Local Similarity 22.5%; Pred. No. 8.2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GNR-----KAAARPL-----CVANEGVGPASRNSGLYNITFYDNCITVLYNPCK 86  
DB 17 GULLLLNVLAPGRSPRLDPAPVCAQGLSCRYANSTCLDDSWIHPKMLTPSSPKNI 76  
QY 87 HVIADQNIITISQACHQVAVT-ILNS-PCALGIEFKGFRVILEELKSEGCOCQ----141  
DB 77 YI-----NLVSSTQHGLVPLVHVEWTLQTDASILEGAELSVLQNTNERLCVRFQF 131  
QY 142 --LILADPQKNSFKTGMSQEPFLNKHFTDYFKVVPFESIKNESNYHPEFFFRAC 199  
DB 132 LSKLQHKRKRFSF-----SHFVDPGEYEVTVHHLFPDIPGDPNHRKSKIIFFVPC 185  
QY 200 D---LILADPDLNACKPFWKPRINI-----SQH-----GSDMQV 230  
DB 186 EDSKNMTTCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLSFSDSENHS 244  
QY 231 SPD-----HAPNTEGFRFFVLYHKLAKH-----GPKRKTCKQEQTTTSCLL 274  
DB 245 CEDVWQKIFAPRQEPFORANTYFISLRFHNCCHHVQVQPP-FSCLND-----CLR 296  
QY 275 QNVSGDVIIEVDVTTTKVHVALRPV--HSP-WA-GPRAVAVTVPLVLISAPATL 330  
DB 297 HAVTVCPVI-----SWT-----VPRPVADYIPLVYGLITLAI-----LLVGSVIVL 341  
QY 331 FTVMKRKKQENIYSHLDESESSSTYTAALPRERAPRPKVFCLYSKQGNHNNVVOG 390  
DB 342 IICMTWRLSGAQEKHGDKSINGILPVADLTPLPLRP-KWIVVISA-DHPLYVEVWLK 399

QY 391 FAYFLDQFGCEVALDWFDSICRGQRENWYOK-----THSQFIIVVCSKGRYFVDK 446  
DB 400 FAOFLITAGTEVALDLLEQVISEVGYMTWVSQKQEMVSNKIIILCSRG-----TQ 454  
QY 447 KNTKHEGG-----GRSGCKGELFVAVSAIAEKLRQAQKSSAALSFKFIAYFYDX 496  
DB 455 AKWKAILGWAPPAVOLRCDHWPAGDLEFTAANNMILDPKRR-----PACFTGYVVCYFSG 509  
QY 497 SC-BGDVPGIILDLSTKYRLADNLPCLSHLHSRDBHGLORPGO--HTRGSRNRTFRSKSG 553  
DB 510 ICSERDVPLENITSRYPLADREEV--YFRIOLEMFEPGGMHVRRLTGDNTLOSFGS 567  
QY 554 RSLVYAICMHHQFIDEEPWFQKQVPSHP-----PPLR--YREPVLEKFGSLVLDVM 606  
DB 568 RQLKAVLRFOEMOTQCPDMFERENLCADQDPLPSLDEEVEDPLLP-GGGIVKQOPL 626  
QY 607 CKPGPESDFCLAVEAAYLGATGPADQSQHSQHGGLDQD-----GEAR 648  
DB 627 VRELPSDGLVWDVCV-----SEESRMALDPQLMPQRELVAHTLQSLVYLPAEQV 677  
QY 649 PALDLSAALQPLLHTVKGSPDMG--RDS-----CIYDSSV--PSSLSLPL-----692  
DB 678 PA---ARVVEPLHLDPDGSAAQOLPMTBDSACPLLGVRNLSILCLPVDSDDLPLCSTPM 734  
QY 693 -----MEGLSTQDTSTSLTESVSSSGSGLEEPPALPKLLSSGSKADLGCRSYIDE 746  
DB 735 MSPDHLQGDAREQLESIMLSVLSQSLQSLQPLESHPR-PEVYLE-----GCTPSEE 784

## RESULT 12

US-08-978-773-2  
Sequence 2, Application US/08978773  
Patent No. 6083906

## GENERAL INFORMATION:

APPLICANT: Troutt, Anthony  
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

COMPUTER: Apple PowerMacintosh  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,773  
FILING DATE:

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

## CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-978-773-2

Query Match 7.6%; Score 306; DB 3; Length 864;



Best Local Similarity 22.5%, Pred. No. 8, 2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRN-----KAAARPL-----CVANEGVGPASNSGLNITFKYDNCITTYLNPVK 86  
DB 17 GWLLLLNVLAPGRASPLLDPPAPVCAQEGSLSCVKNSTCLDDSHIHPKMLTSSPKN 76  
QY 87 HVIADQNTISQYACHQAVT--ILWS--PGALGIEFLKFRVLELKSQCOO---141  
DB 77 YI-----NLSVSTOHLGELVPLVHVTLOTDSILYLEGAELSVLQNLTRLCVAFQ 131  
QY 142 --LILKDPQLNASSFKRTGMSQFFLNKFTDYFVAVPFPSSIKNESNYHFFFRAC 199  
DB 132 LSLMLQHRKRRFSE-----SHEVVDQGEVETVHHLKPIPOGDPNHSKIIFVPC 185  
QY 200 D---LLQPDNLACKPFWKPNLNI-----SOH-----GSDMQV 230  
DB 186 EDSKMTTSCVSSGSLMDP--NITVETLOTQHLRVDTLWNESTPYOVLLSEFSSENH 244  
QY 231 SFD-----HAPNFGFRFFYLHYLKEH---GPPKRTCKOQOTTTTSCLL 274  
DB 245 CFVWVKQIFAPROEERFORANVTTLTKSFHWCCHHVQVQPP--FSSCLND-----CLR 296  
QY 275 QNVSQDGYIIELVDDTNTTRKVMHYALKV--HSP--WA--GPIRAVAITVPLVVISAFATL 330  
DB 237 HAVTVPCPI-----SNTT-----VPEKVDYIPLAVYGLITLAI-----LLVGSVIVL 341  
QY 331 FTVMCKKQOENIYSHLDESSSESTYTAALPRRLPRKPVLCYSSKDGQNMNVVOC 390  
DB 342 IICHTWRLSGADQEKHGDSKINGILPVADLTPLPPLRPR--KMWIVYSA--DHPLEVEVLK 399  
QY 391 FAYPLQDFCGCEVALDLDWEDFSLCRGOREWQIQR-----THESQFIIVVCSKGMKYFVK 446  
DB 400 FAQLITACGTVEALDLEEQVISEVGVMTWVSRQKQWESKIIILCSRG-----TQ 454  
QY 447 KNYHKRG-----GRGSGKGLFVAVSAIAEKLQAKQSSSAALSKEFLAVFEDY 496  
DB 455 AKWAILGNAEPAVOLCRDHWKHPAGDLPFAAMNMLDPFR-----PACFTGYVVCFSG 509  
QY 497 SC--BDVPGILDTSTYKLMNDLPQLCSHLHSRDHGLQEPGQ--HTROGSRNTRFSKG 553  
DB 510 ICSDRVDPLNITRYLDRDREEV--YFRDIDLEMFEPGRMHVRELTDGNYLQSPSG 567  
QY 534 RSLVAICNNHQFIDEEPQWFKQFVFPHP-----PPLR---YREPVEKFDGSLVNDVM 606  
DB 568 ROLKEAVLRQEMOTQCPDWPFRNLCLADGQDLSLDEEVFEDPLPP--GGGIYKQOPL 626  
QY 607 CKPGPESDFCLVAAVILGATGPADQSHESQHGGLDQ-----GEAR 648  
DB 627 VRELP--SDGCLVYVCV-----SEESRNAKLPQALPQRELVAHTLQSWLPAEQV 677  
QY 649 PALGSAALQPLILHYKAGSPDMP--RDS-----GIYDSSV---PSSLSLPL-----692  
DB 678 PA---ATVPEPLHLPDGGGAQAQPLPTEDESEACPLIGVORNSIILCPVDSDDLPLCSTPM 734  
QY 693 -----MEGLSTQDTSTSLTESVSSGGLGEEPPALPSKLLSGGSKADLCGRSYTDE 746  
DB 735 MSPDLQAGDAREQLESLMYSVLOOSLGOPLESMP--PEVYLE-----OCTPSEEE 784

## RESULT 13

US-09-022-253-2  
Sequence 2, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fabislow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street

CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-253-2

Query Match 7.6%, Score 306; DB 3; Length 864;

Best Local Similarity 22.5%, Pred. No. 8, 2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRN-----KAAARPL-----CVANEGVGPASNSGLNITFKYDNCITTYLNPVK 86  
DB 17 GWLLLLNVLAPGRASPLLDPPAPVCAQEGSLSCVKNSTCLDDSHIHPKMLTSSPKN 76  
QY 87 HVIADQNTISQYACHQAVT--ILWS--PGALGIEFLKFRVLELKSQCOO---141  
DB 77 YI-----NLSVSTOHLGELVPLVHVTLOTDSILYLEGAELSVLQNLTRLCVAFQ 131  
QY 142 --LILKDPQLNASSFKRTGMSQFFLNKFTDYFVAVPFPSSIKNESNYHFFFRAC 199  
DB 132 LSLMLQHRKRRFSE-----SHEVVDQGEVETVHHLKPIPOGDPNHSKIIFVPC 185  
QY 200 D---LLQPDNLACKPFWKPNLNI-----SOH-----GSDMQV 230  
DB 186 EDSKMTTSCVSSGSLMDP--NITVETLOTQHLRVDTLWNESTPYOVLLSEFSSENH 244  
QY 231 SFD-----HAPNFGFRFFYLHYLKEH---GPPKRTCKOQOTTTTSCLL 274  
DB 245 CFVWVKQIFAPROEERFORANVTTLTKSFHWCCHHVQVQPP--FSSCLND-----CLR 296  
QY 275 QNVSQDGYIIELVDDTNTTRKVMHYALKV--HSP--WA--GPIRAVAITVPLVVISAFATL 330  
DB 237 HAVTVPCPI-----SNTT-----VPEKVDYIPLAVYGLITLAI-----LLVGSVIVL 341  
QY 331 FTVMCKKQOENIYSHLDESSSESTYTAALPRRLPRKPVLCYSSKDGQNMNVVOC 390  
DB 342 IICHTWRLSGADQEKHGDSKINGILPVADLTPLPPLRPR--KMWIVYSA--DHPLEVEVLK 399  
QY 391 FAYPLQDFCGCEVALDLDWEDFSLCRGOREWQIQR-----THESQFIIVVCSKGMKYFVK 446  
DB 400 FAQLITACGTVEALDLEEQVISEVGVMTWVSRQKQWESKIIILCSRG-----TQ 454

QY 447 KNYKHGG-----GRSGKGFELVAVSAIAEKLROAKQSSAALSXFIATYFDY 496  
 DB 455 AKWAILGWAEPVQLRCDHWKPADGLFTAMNMLPDKR-----PACFTYVVCYFSG 509  
 QY 497 SC-EGDVPGLDSTKRYLMDNLPOLCSHLMSRDHGLQEPG--HTRGSRNRYFRSKSG 553  
 DB 510 ICSEKVPDLNITSRYPLMDRFEV--YFRIQDLNFEPRHHRVRLTGDNYLQSPSG 567  
 QY 554 RSLYVAICNMHOFIDEPWFKEQFVFPHP-----PPLR---YREPVEKFDGLVLDVYM 606  
 DB 568 RQLKAVLRFQEWOTQCPWFERNICLADGQDLPDLDEVEFDPLPP--GGGIVKQOPL 626  
 QY 607 CKPGPESDFCLKVAEVLGATGPADSHESQHGGLDQ-----GEAR 648  
 DB 627 VRELPSDGLVVDVY-----SEESRNKLDLPQWQRELVAHTLQSNVLPREQV 677  
 QY 649 PALDGSAAOLPLHTYKAGSPSDMP--RDS-----GIYDSSV--PSSELSLPL----- 692  
 DB 678 PA---ARVVEPLHLPDGSAAQLPMTEDSEACPLGVQRNSLCLPVDSDPLCTPM 734  
 QY 693 -----MEGLSTDQETSSLTESVSSSGLGEPEPPALPSKLLSSGCKADIGCKSYTDE 746  
 DB 735 MSPDHLDQDAREQLESMLSVLQSLSGOPLESWPR-PEVYLE-----GCTPSEEE 784

RESULT 14  
 US-09-022-260-2  
 ; Sequence 2, Application US/09022260  
 ; Patent No. 6100235  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,260  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/620,694  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/410,535  
 ; FILING DATE: 23 MARCH 1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 864 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-09-022-260-2  
 Query Match 7.64; Score 306; DB 3; Length 864;  
 Best Local Similarity 22.54; Pred. No. 8.2e-23;  
 Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;  
 QY 40 GHRM-----KAAARPL-----CVANEGVGPASRNSGLNYITFYDNTTYLAPVK 86  
 DB 17 GMLLLNLVLAAGRASPRLDPPAPVCAQGLSCRKVNKSTCLDDSWIHPKMLTSPSPKNI 76  
 QY 87 HVIADAQNIITISQACHDQAVT--ILWS--PCALGIGISFLAGFVLEELKESGROCOQ--- 141  
 DB 77 YI-----NLSVSTQHGELVPLVHVMTLQDAISILYEGASLVGLANTNERLCVKFO 131  
 QY 142 ---LLLKDPKOLNSFKRTGKESQPELNKMTETFEYKVVPPSPKSNENYHFFETTRAC 199  
 DB 132 LSWIQHHRKRRTSF-----SHFVDPQGEYEVYVHLPKPIPDGDNHKSIIIFVDC 185  
 QY 200 D---LLQPDMLACKPFWPRNLT---SQH-----GSDMOV 230  
 DB 186 EDSKMTTSCVSSGSLWOP--NITVETLDTQHLRVOFTLWNESTPYQVLLSEFSDESHS 244  
 QY 231 SFD-----HAPNFGFRFFYLHYLKLKHE---GPEKRTCKQEQTTETTSCLL 274  
 DB 245 CFQVYVQIFAPRQEEFHQANVTFTLSKFNWCHHHVQVQPF--FSSCLND-----CLR 296  
 QY 275 QNVSPGDYIIELVDNTTKVMHYALKPV--HSP-WA-GPIRAVAITVPLWVISAFAFL 330  
 DB 297 HAVTVPCPVI-----SNTI-----VPRVADYIPLWVYGLITLAI-----LLVGSVIVL 341  
 QY 331 FTYMCKKQOENIYSHLDSESESTYTAALPRERPRPRKPVFLCYCKSGKQGNHNVQC 390  
 DB 342 ICTWRLSGADQEKGGDSKINGILPVADLTTPPLRPR-KWIIYVSA-DHPLYVEVULK 399  
 QY 391 FAYFQDPGCGEVALDLMEDFSLCREGQREWVOK-----IHESQFIIVVCSKGMKIFYDVK 446  
 DB 400 FAFGLITAGTEVALDOLLEEQVISEVGVMTVWSRQKQEMVSNKIIILCSRG-----TQ 454  
 QY 447 KNYKHGG-----GRSGKGFELVAVSAIAEKLROAKQSSAALSXFIATYFDY 496  
 DB 455 AKWAILGWAEPVQLRCDHWKPADGLFTAMNMLPDKR-----PACFTYVVCYFSG 509  
 QY 497 SC-EGDVPGLDSTKRYLMDNLPOLCSHLMSRDHGLQEPG--HTRGSRNRYFRSKSG 553  
 DB 510 ICSEKVPDLNITSRYPLMDRFEV--YFRIQDLNFEPRHHRVRLTGDNYLQSPSG 567  
 QY 554 RSLYVAICNMHOFIDEPWFKEQFVFPHP-----PPLR---YREPVEKFDGLVLDVYM 606  
 DB 568 RQLKAVLRFQEWOTQCPWFERNICLADGQDLPDLDEVEFDPLPP--GGGIVKQOPL 626  
 QY 607 CKPGPESDFCLKVAEVLGATGPADSHESQHGGLDQ-----GEAR 648  
 DB 627 VRELPSDGLVVDVY-----SEESRNKLDLPQWQRELVAHTLQSNVLPREQV 677  
 QY 649 PALDGSAAOLPLHTYKAGSPSDMP--RDS-----GIYDSSV--PSSELSLPL----- 692  
 DB 678 PA---ARVVEPLHLPDGSAAQLPMTEDSEACPLGVQRNSLCLPVDSDPLCTPM 734  
 QY 693 -----MEGLSTDQETSSLTESVSSSGLGEPEPPALPSKLLSSGCKADIGCKSYTDE 746  
 DB 735 MSPDHLDQDAREQLESMLSVLQSLSGOPLESWPR-PEVYLE-----GCTPSEEE 784

RESULT 15  
 US-09-022-259-2  
 ; Sequence 2, Application US/09022259  
 ; Patent No. 6191104  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10

CORRESPONDENCE-ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,259  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-259-2

Query Match 7.68; Score 306; DB 4; Length 864;  
 Best Local Similarity 22.58; Pred. No. 8.2e-23;  
 Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GRM-----KAARPRL-----CVANEGVGASRNGLNITFYKDNCTYTLNVPVK 86  
 DB 17 GMLLLNVLAPGRASPRLLDFPAPVCAQGLSCVRKNSCTCLDSDWIHPKNTLTPSPRNI 76  
 QY 87 HVIADQNTISQYACHDQVAVT-ILWS-PGALGIEFLKGFVILVELKSEKQCOQ--- 141  
 DB 77 VI-----NLVSSTQHGELVPVLHVENTLQDASILYLEGAESVLQATNLERLCVKRFQ 131  
 QY 142 -LLKDPKQLASSKFKGMSQPFNMKFEYDYKVVPPSPKSNKSHYHFFPTTAC 199  
 DB 132 LSNLQHRRKWRFSF-----SHFVDPQGETEVTHLPRPDPGDPNHSKIIFVDC 185  
 QY 200 D-----LLQDPNKLACPFKPRNLMI-----SQH-----GSDMQV 230  
 DB 186 EDSKMKMTTSCVSSGSLMDP-NITVETLDTOLRLVDFTLNNESTPYQVLLSEFSSENHS 244  
 QY 231 SFD-----HAPHNFGFRFFLYHLKHE---GPKRKTCKOBQTTTETSCLL 274  
 DB 245 CFDVVKQIFAPROEFHQKRVNVTFLSKFWCHHVVQVQPF-FSSCLND-----CLR 296  
 QY 275 QNVSQGYITELVDQNTTRKVMHAKPV--HSP-WA-GPIRAVAITVPLAVISAFATL 330  
 DB 297 HAVTVPCPI-----SNT-----VPKPVADYIPLNVTGLITLAI-----LLVGSVIL 341  
 QY 331 FVWCKKQENIYSHLDESSSESTYTAALPRELRPRPKVFLCYSSKDGQNHNVQC 390  
 DB 342 IICMTWRLSGAQOEKGDDSKINGILPVDLTTPPLPR-KWMIYVSA-DHPLYIYEWLK 399  
 QY 391 FAYFLQDFCCGEVALDLWEDFSLCREQREWVIQK-----IHESQFIIVVCSKGMKIFYDK 446

DB 400 FAQLITACGTEVALDLLEQVISEVGVMVTSRQKQEMVESKIIILCSRG-----TO 454  
 QY 447 KNYKHEGG-----GRGCKGELFIVAVSAIAEKLKROAKOSSAALSKEIATVEDY 496  
 DB 455 AKWKAILHABEPAVOLRCDHWKPGDLTAMNNILPDFR-----PACFGTYVVCYFSG 509  
 QY 497 SC-EGDVPGLDLSKYRLMDNLPQLCSHLHSRORGLQEPQ--HYTGRSRNRTFRSKSG 553  
 DB 510 ICSEKVPDLNITSRYPLMDREEV--YFRIQLEMFEGRMHVRHRELTGDTLQSPSG 567  
 QY 554 RSLYVACHMHOFIDEEPWFQKQFVPPHP--PPLR--YREPVLEKFGSLVLDVNM 606  
 DB 568 ROLKEAVLRFOEMQTCQPMFERENCLADGQDLPSLDEEVEFDPPLPP-OGGIVKQOPL 626  
 QY 607 CKPGPESDFCLAKVEAAVLGATGPADSOHESQGGGLDQD-----GEAR 648  
 DB 627 VRELPSDGLVVDVCV-----SEESRMALIDPOLMPORELVAHTLQSWVLPARQV 677  
 QY 649 PALDGSAAQLPPLLHTYKAGSPDMP--RDS-----GIYDSV--PSSELSLPL----- 692  
 DB 678 PA---AHVVEPLHLDPGSGAAQOLPMTEDSEACPLGQVORNSTLCIPVDSDDLPLCSTPM 734  
 QY 693 ---MEGLSTQDTSTSLTESYSSSGLGEEEPALPSPKLLSSGSKRADLGCRSYDE 746  
 DB 735 MSPDHQGDAREQLESLMLSVLQOSSLGQPLESWPR-FEVYLE-----GCTPSEEE 784

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 Job time : 34 secs

GenCore version 5.1.4.p5.4578  
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OM protein: protein search, using sw model

Run on: May 6, 2003, 13:44:51, Search time 24 Seconds  
(without alignments)  
2707.245 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPVLQLCSVFTTNACLSGSLAANGSGRAGDTCGRWKAARPRCLVANEVGP

Scoring table: BLOSUM62

Gapop: 10.0, Capext: 0.5

Searched: 328255 seqs, 8628685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

Published Applications: AA.\*  
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2: /cgn2\_6/ptodata/1/pubaa/RCT\_NEW\_PUB pep.\*  
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14: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4013	100.0	753	9	US-09-912-157-2
2	4003	99.8	753	9	US-09-912-157-5
3	3925	97.8	739	9	US-09-912-157-8
4	3901	97.2	738	10	US-09-809-567-2
5	3703	92.3	728	9	US-09-874-503-18
6	3703	92.3	728	9	US-10-000-157-18
7	3703	92.3	728	9	US-09-816-744-18
8	3703	92.3	728	9	US-09-747-259-18
9	3703	92.3	728	9	US-09-908-827-18
10	3387	84.4	739	9	US-09-912-157-12
11	312	7.8	810	10	US-09-809-567-3
12	312	7.8	866	12	US-09-778-971-9
13	312	7.8	866	12	US-10-033-522-1
14	135.5	3.4	502	9	US-09-874-503-12
15	135.5	3.4	502	9	US-10-000-157-12
16	135.5	3.4	502	9	US-10-063-547-158
17	135.5	3.4	502	9	US-09-816-744-12
18	135.5	3.4	502	9	US-09-747-259-12
19	135.5	3.4	502	9	US-10-174-590-400

#### ALIGNMENTS

##### RESULT 1

US-09-912-157-2

; Sequence 2, Application US/09912157

; Patent No. US20020165348A1

GENERAL INFORMATION:

APPLICANT: Kuestner, Scott R.

APPLICANT: Kuestner, Scott R.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/09/912.157

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 753

TYPE: PRT

ORGANISM: Homo sapiens

US-09-912-157-2

Query Match 100.0%, Score 4013, DB 9, Length 753;  
Best Local Similarity 100.0%, Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPVLQLCSVFTTNACLSGSLAANGSGRAGDTCGRWKAARPRCLVANEVGP	60
Db	1	MAPVLQLCSVFTTNACLSGSLAANGSGRAGDTCGRWKAARPRCLVANEVGP	60
Qy	61	ASRNSGLNITFKYDNCITTLAPVGRKHVIAQAQNTISQYACHDQVATILWSPGALGIE	120
Db	61	ASRNSGLNITFKYDNCITTLAPVGRKHVIAQAQNTISQYACHDQVATILWSPGALGIE	120
Qy	121	FLKGRVILELAKSEGRCQQLILADPKQLNSFKRTGMESOFFLNKMFETDFYKVPFF	180
Db	121	FLKGRVILELAKSEGRCQQLILADPKQLNSFKRTGMESOFFLNKMFETDFYKVPFF	180
Qy	181	PSIKNESNTHFFPTFRACDLQLLPDLNACFPKPKPNLNLSQHSQDMQVDFHAPNFG	240
Db	181	PSIKNESNTHFFPTFRACDLQLLPDLNACFPKPKPNLNLSQHSQDMQVDFHAPNFG	240
Qy	241	FRFPIYKALKEHGPFRKTCQBOTTTTSCILLQNWSPDYIIELVDYDITNTRKVAHYA	300
Db	241	FRFPIYKALKEHGPFRKTCQBOTTTTSCILLQNWSPDYIIELVDYDITNTRKVAHYA	300

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Db 241 PRFFYLHYLKHGSPKFKCKQKQBTETTSCLLQNVSPGDYIILEYDDTNTTRKVMHYA 300
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
QY 361 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
Db 361 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
QY 421 WYIQIHESOFIIVVCSKGMKYFYDKKNTYKHGSGRGSGKGELELVAVSAIAEKLRQAK 480
Db 421 WYIQIHESOFIIVVCSKGMKYFYDKKNTYKHGSGRGSGKGELELVAVSAIAEKLRQAK 480
QY 481 SSSAALSKEFTAVFYDSCGDPVGLDLSLTKYRLMDNLPQLCSHLHSRDRHGLQEPQHT 540
Db 481 SSSAALSKEFTAVFYDSCGDPVGLDLSLTKYRLMDNLPQLCSHLHSRDRHGLQEPQHT 540
QY 541 QGSRNRTFRSKGRSLYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLKFDGSL 600
Db 541 QGSRNRTFRSKGRSLYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLKFDGSL 600
QY 601 VLVNVMCKPSPDSFCLKVEAAVLGATGADSGHSGHGGGLDQGEARPALDGSAAQLPL 660
Db 601 VLVNVMCKPSPDSFCLKVEAAVLGATGADSGHSGHGGGLDQGEARPALDGSAAQLPL 660
QY 661 LHTVKAQSPDMPRDGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSSGLGEE 720
Db 661 LHTVKAQSPDMPRDGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSSGLGEE 720
QY 721 PPALPSKLLSSGCKADLCRSYTDDELHAAVPL 753
Db 721 PPALPSKLLSSGCKADLCRSYTDDELHAAVPL 753

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## RESULT 2

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US-09-912-157-5
; Sequence 5, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912.157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-5

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Query Match 99.8%; Score 4003; DB 9; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MAPWTLQCSVFFTVNACLSQLAAGGSGRAGADTCGWRKKAARPRCLVANEGVGP 60
Db 1 MAPWTLQCSVFFTVNACLSQLAAGGSGRAGADTCGWRKKAARPRCLVANEGVGP 60
QY 61 ASRNSGLYNTFYKDYNTYLNPKVHVADAGNITISQYACHQDVAVTILSPGALGIE 120
Db 61 ASRNSGLYNTFYKDYNTYLNPKVHVADAGNITISQYACHQDVAVTILSPGALGIE 120
QY 121 FLKGRFVILEELKSEGRQCOQLIKDPQLNSSFRTKGTGMSQPLANKFETDYFKVVP 180
Db 121 FLKGRFVILEELKSEGRQCOQLIKDPQLNSSFRTKGTGMSQPLANKFETDYFKVVP 180
QY 181 PSIKNESNHPFFTRACDILLOPNLACKPFWRPNRINTSQRGSDQMVSEDHAPHNG 240

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Db 181 PSIKNESNHPFFTRACDILLOPNLACKPFWRPNRINTSQRGSDQMVSEDHAPHNG 240
QY 241 PRFPYLHYLKHGSPKFKCKQKQBTETTSCLLQNVSPGDYIILEYDDTNTTRKVMHYA 300
Db 241 PRFPYLHYLKHGSPKFKCKQKQBTETTSCLLQNVSPGDYIILEYDDTNTTRKVMHYA 300
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
QY 361 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
Db 361 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKQKQENIYSHLDESSSESTYTA 360
QY 421 WYIQIHESOFIIVVCSKGMKYFYDKKNTYKHGSGRGSGKGELELVAVSAIAEKLRQAK 480
Db 421 WYIQIHESOFIIVVCSKGMKYFYDKKNTYKHGSGRGSGKGELELVAVSAIAEKLRQAK 480
QY 481 SSSAALSKEFTAVFYDSCGDPVGLDLSLTKYRLMDNLPQLCSHLHSRDRHGLQEPQHT 540
Db 481 SSSAALSKEFTAVFYDSCGDPVGLDLSLTKYRLMDNLPQLCSHLHSRDRHGLQEPQHT 540
QY 541 QGSRNRTFRSKGRSLYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLKFDGSL 600
Db 541 QGSRNRTFRSKGRSLYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLKFDGSL 600
QY 601 VLVNVMCKPSPDSFCLKVEAAVLGATGADSGHSGHGGGLDQGEARPALDGSAAQLPL 660
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QY 661 LHTVKAQSPDMPRDGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSSGLGEE 720
Db 661 LHTVKAQSPDMPRDGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSSGLGEE 720
QY 721 PPALPSKLLSSGCKADLCRSYTDDELHAAVPL 753
Db 721 PPALPSKLLSSGCKADLCRSYTDDELHAAVPL 753

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## RESULT 3

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US-09-912-157-8
; Sequence 8, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912.157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8

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Query Match 97.8%; Score 3925; DB 9; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
QY 1 MAPWTLQCSVFFTVNACLSQLAAGGSGRAGADTCGWRKKAARPRCLVANEGVGP 60
Db 1 MAPWTLQCSVFFTVNACLSQLAAGGSGRAGADTCGWRKKAARPRCLVANEGVGP 60
QY 61 ASRNSGLYNTFYKDYNTYLNPKVHVADAGNITISQYACHQDVAVTILSPGALGIE 120
Db 47 ASRNSGLYNTFYKDYNTYLNPKVHVADAGNITISQYACHQDVAVTILSPGALGIE 106
QY 121 FLKGRFVILEELKSEGRQCOQLIKDPQLNSSFRTKGTGMSQPLANKFETDYFKVVP 180

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 DB 167 PSIKNESYHPFFETTRACDILLOPNLACKPFWKPRNLNISQHSQSDQVDFHAPNFG 226  
 QY 241 FRFFYLHYKLKHEGPFKRTCKQBTETTSCLLQNSPGDYIIELVDDTNTTKVMHYA 300  
 DB 227 FRFFYLHYKLKHEGPFKRTCKQBTETTSCLLQNSPGDYIIELVDDTNTTKVMHYA 286  
 QY 301 LKPVHSPWAGPTRAIVATVPLWISAFATLFTVWCRKKQENIYSHLDEESSESTYTA 360  
 DB 287 LKPVHSPWAGPTRAIVATVPLWISAFATLFTVWCRKKQENIYSHLDEESSESTYTA 346  
 QY 361 LPRERLRPRPKVFLCYSSKQGNHNVVOCFAYFLQDFCCGEVALDLWEDFSLCREGORE 420  
 DB 347 LPRERLRPRPKVFLCYSSKQGNHNVVOCFAYFLQDFCCGEVALDLWEDFSLCREGORE 406  
 QY 421 WYQKIHESQFIIVVCSKGMKYFDKNTKHKGGSGKGEFLFVAVSAEKLRAQK 480  
 DB 407 WYQKIHESQFIIVVCSKGMKYFDKNTKHKGGSGKGEFLFVAVSAEKLRAQK 466  
 QY 481 SSSAALSKFIATVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSRDLGLOPQGR 540  
 DB 467 SSSAALSKFIATVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSRDLGLOPQGR 526  
 QY 541 QGSRRTYFRSKSGSLYVAICNMHQFIDEEPWFKEQFVDFHPPPLRYREPVLKFDOSGL 600  
 DB 527 QGSRRTYFRSKSGSLYVAICNMHQFIDEEPWFKEQFVDFHPPPLRYREPVLKFDOSGL 586  
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 QY 721 PPALPSKLLSSGCKADLGCRTYTDHHAVALP 753  
 DB 707 PPALPSKLLSSGCKADLGCRTYTDHHAVALP 739

## RESULT 4

US-09-809-567-2

; Sequence 2, Application US/09809567

; Patent No. US20020045213A1

; GENERAL INFORMATION:

; APPLICANT: Jinq-Shuguan

; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

; FILE REFERENCE: 01017/36916A US/09/809,567

; CURRENT FILING DATE: 2001-03-15

; PRIOR FILING DATE: 09/724,460

; PRIOR FILING DATE: 2000-11-28

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 738

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-809-567-2

Query Match 97.28; Score 3901; DB 10; Length 738;  
 Best Local Similarity 97.6%; Pred. No. 0;  
 Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;  
 QY 1 MAPWLQCSVFYFTYVACNLGSQLVAAGSGRGAGDTCGRMKAAARPRICLVANEGVP 60  
 DB 1 MAPWLQCSVFYFTYVACNLGSQLVAAGSGRGAGDTCGRMKAAARPRICLVANEGVP 46

QY 61 ASRNSGLNTYFKYDNCTTYLNVGSKRVYADAOQNTISQYACHQDVAVTILWSPALGIE 120  
 DB 47 ASRNSGLNTYFKYDNCTTYLNVGSKRVYADAOQNTISQYACHQDVAVTILWSPALGIE 106  
 QY 121 FLAGFRVILEELKSGRQCQQLILKDPKOLNSFKRTGMSQFFLNKMFETDYFVKVVPF 180  
 DB 107 FLAGFRVILEELKSGRQCQQLILKDPKOLNSFKRTGMSQFFLNKMFETDYFVKVVPF 166  
 QY 181 PSIKNESYHPFFETTRACDILLOPNLACKPFWKPRNLNISQHSQSDQVDFHAPNFG 240  
 DB 167 PSIKNESYHPFFETTRACDILLOPNLACKPFWKPRNLNISQHSQSDQVDFHAPNFG 226  
 QY 241 FRFFYLHYKLKHEGPFKRTCKQBTETTSCLLQNSPGDYIIELVDDTNTTKVMHYA 300  
 DB 227 FRFFYLHYKLKHEGPFKRTCKQBTETTSCLLQNSPGDYIIELVDDTNTTKVMHYA 286  
 QY 301 LKPVHSPWAGPTRAIVATVPLWISAFATLFTVWCRKKQENIYSHLDEESSESTYTA 360  
 DB 287 LKPVHSPWAGPTRAIVATVPLWISAFATLFTVWCRKKQENIYSHLDEESSESTYTA 346  
 QY 361 LPRERLRPRPKVFLCYSSKQGNHNVVOCFAYFLQDFCCGEVALDLWEDFSLCREGORE 420  
 DB 347 LPRERLRPRPKVFLCYSSKQGNHNVVOCFAYFLQDFCCGEVALDLWEDFSLCREGORE 406  
 QY 421 WYQKIHESQFIIVVCSKGMKYFDKNTKHKGGSGKGEFLFVAVSAEKLRAQK 480  
 DB 407 WYQKIHESQFIIVVCSKGMKYFDKNTKHKGGSGKGEFLFVAVSAEKLRAQK 466  
 QY 481 SSSAALSKFIATVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSRDLGLOPQGR 540  
 DB 467 SSSAALSKFIATVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSRDLGLOPQGR 526  
 QY 541 QGSRRTYFRSKSGSLYVAICNMHQFIDEEPWFKEQFVDFHPPPLRYREPVLKFDOSGL 600  
 DB 527 QGSRRTYFRSKSGSLYVAICNMHQFIDEEPWFKEQFVDFHPPPLRYREPVLKFDOSGL 586  
 QY 601 VLDNVMCKPGPESDFCLKVEANVLGATGPADSOHESQHGGLDQGEARPALDGSALLOPL 660  
 DB 587 VLDNVMCKPGPESDFCLKVEANVLGATGPADSOHESQHGGLDQGEARPALDGSALLOPL 646  
 QY 661 LHTVKGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTQDTETSSLTSSSSGLGEEE 720  
 DB 647 LHTVKGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTQDTETSSLTSSSSGLGEEE 706  
 QY 721 PPALPSKLLSSGCKADLGCRTYTDHHAVALP 752  
 DB 707 PPALPSKLLSSGCKADLGCRTYTDHHAVALP 738

## RESULT 5

US-09-874-503-18

; Sequence 18, Application US/09874503

; Patent No. US2002017188A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Hymowitz, Sarah G.

; APPLICANT: Tamas, Daniel

; APPLICANT: Starovasnik, Melissa A.

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REFERENCE: P1381R1C1P3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US/60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US/60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US/60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US/60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US/60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US/60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US/60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US/60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US/60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US/60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US/60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US/60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US/60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US/09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US/09/854,280  
PRIOR FILING DATE: 2001-05-20  
PRIOR APPLICATION NUMBER: US/09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US/09/747,259  
PRIOR FILING DATE: 2000-12-30  
PRIOR APPLICATION NUMBER: US/09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US/09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US/09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US/09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US/PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US/PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US/PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US/PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US/PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US/PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US/PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US/PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US/PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US/PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: US/PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US/PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US/PCT/US99/05028  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18

LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-874-503-18  
Query Match  
Best Local Similarity 96.7%; Pred. No. 2.9e-307; Length 728;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;  
QY 42 RKAAARPRCLVANE-GVGPASRNSGLNITFKYDNCNTYLNVPVGRHVTAQAQNTISQY 100  
DB 3 RASAGVPALFVSGQGVGPASRNSGLNITFKYDNCNTYLNVPVGRHVTAQAQNTISQY 62  
QY 101 ACHDOAVAVTILWSPGALGIEFLKGFVILEELKSGRQCQQLILKDPKOLANSFRKTGME 160  
DB 63 ACHDOAVAVTILWSPGALGIEFLKGFVILEELKSGRQCQQLILKDPKOLANSFRKTGME 122  
QY 161 SQPLNKKFETDYFKVYVPPFSIKNESYHPPFFTRACDILLQPDNLACKPFWKPRNLN 220  
DB 123 SQPLNKKFETDYFKVYVPPFSIKNESYHPPFFTRACDILLQPDNLACKPFWKPRNLN 182  
QY 221 ISQ-----HGSOMQVSFDHAPHNFGFRFFLYLHKHGGPKRKTCKQSTT 267  
DB 183 ISQSGDMQVSFDHAPHNFGFRFFLYLHKHGGPKRKTCKQSTT 242  
QY 268 ETTSCLLQNVSPGDIYIELVDYNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 337  
DB 243 ETTSCLLQNVSPGDIYIELVDYNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302  
QY 328 ATLFTVMCKRKKQENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYSSKDGQNMNV 387  
DB 303 ATLFTVMCKRKKQENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYSSKDGQNMNV 362  
QY 388 VOCFAVFLQDPCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSGKMYFYDKK 447  
DB 363 VOCFAVFLQDPCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSGKMYFYDKK 422  
QY 448 NYRKHGGGRSGKGLFLVAVSAIAEKLRQAKSSAALSKEFTANTFYSCGGOVPGILD 507  
DB 423 NYRKHGGGRSGKGLFLVAVSAIAEKLRQAKSSAALSKEFTANTFYSCGGOVPGILD 482  
QY 508 LSTKRYLMDNLPQLCSHLHSDHGLQEPQOHTROGSRNRYFRSKSGSLYVAICNMHOFTI 567  
DB 483 LSTKRYLMDNLPQLCSHLHSDHGLQEPQOHTROGSRNRYFRSKSGSLYVAICNMHOFTI 542  
QY 568 DEEDPMFEKQFVFPFPPPLRYREPVLKEDFSLVNDVMCKPGPESDFCLKVEAAVLGAT 627  
DB 543 DEEDPMFEKQFVFPFPPPLRYREPVLKEDFSLVNDVMCKPGPESDFCLKVEAAVLGAT 602  
QY 628 GPADSOHESOHGGLDQDGEARPAALQPLHTVTKAGSPDSMDPDSGIYDSSVPSSE 687  
DB 603 GPADSOHESOHGGLDQDGEARPAALQPLHTVTKAGSPDSMDPDSGIYDSSVPSSE 662  
QY 688 LSLPMEGLSTDTQETSSLTESVSSSGIGEEPPALPSKLLSSGCKADLGCSTYDEL 747  
DB 663 LSLPMEGLSTDTQETSSLTESVSSSGIGEEPPALPSKLLSSGCKADLGCSTYDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

RESULT 6  
US-10-000-157-18  
; Sequence 18, Application US/10000157  
; Publication No. US20020182673A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul L.  
; APPLICANT: Grimaldi, J.Christopher





Db 483 LSTKYLMDNLPCLSHLSDRGLEQPCQHTROGSRNRYFRSKGSRSLYVAICNMHQFI 542  
 QY 568 DEEPDWFKEQFVPPHPPPLRYREPVLKEDSLVNDVNCPCGPEDECLKVAEAVLGAT 627  
 Db 543 DEEPDWFKEQFVPPHPPPLRYREPVLKEDSLVNDVNCPCGPEDECLKVAEAVLGAT 602  
 QY 638 GPADSOHESQHGGLDQDGEARPALDGSAAALQPLHHTVKAGSPDMRPSGSIYDSSVPSSE 687  
 Db 603 GPADSOHESQHGGLDQDGEARPALDGSAAALQPLHHTVKAGSPDMRPSGSIYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDQETSSLSVESSSSGLGEERPPALPSKLLSSGCKADLCGRSYTDEL 747  
 Db 663 LSLPLMEGLSTDQETSSLSVESSSSGLGEERPPALPSKLLSSGCKADLCGRSYTDEL 722  
 QY 748 HAVAPL 753  
 Db 723 HAVAPL 728

## RESULT 7

US-09-816-744-18  
 ; Sequence 18, Application US/09816744  
 ; Publication No. US20030003546A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Ranzhong  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: VanLookeren, Menno  
 ; APPLICANT: Vandlen, Richard  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Yansura, Daniel  
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C1P2(US)  
 ; CURRENT APPLICATION NUMBER: US/09/816.744  
 ; CURRENT FILING DATE: 2001-03-22  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SEQ ID NO 18  
 ; LENGTH: 728  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-09-816-744-18

Query Match 92.3%; Score 3703; DB 9; Length 728;  
 Best Local Similarity 96.7%; Pred. No. 2.9e-307;  
 Matches 705; Conservative 2; Mismatches 8; Indels 14; Gaps 2;  
 QY 42 RKAARPRCLVANE-GVGPASRNSGLNITFYKDYDNCITTLNVPVGRHVIAQAQNTISQY 100  
 Db 3 RASASGVPAFLVSGQGVGPASRNSGLNITFYKDYDNCITTLNVPVGRHVIAQAQNTISQY 62  
 QY 101 ACHDQAVTILMSPCALGIEFLKAGFRVILEELKSEGRCQOOLILDKPKQLNSSEKRTGME 160  
 Db 63 ACHDQAVTILMSPCALGIEFLKAGFRVILEELKSEGRCQOOLILDKPKQLNSSEKRTGME 122  
 QY 161 SDFPLNKKETDYFVKVVPVPSLKNSNHYHFFETRACDLILQPDNLCKPFPKPNLN 220  
 Db 123 SDFPLNKKETDYFVKVVPVPSLKNSNHYHFFETRACDLILQPDNLCKPFPKPNLN 182  
 QY 221 ISQ-----HSGDMQVSDHAPHNPGFRFFYLHKLKHGFPKRTCKQSQTT 267  
 Db 183 ISQHGDMQVSDHAPHNPGFRFFYLHKLKHGFPKRTCKQSQTT 242

QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRVMHYALKPVHSPMAGPIRAVAITVPLVVISAF 327  
 Db 243 EMTSCLLQNVSPGDYIIELVDDTNTTRVMHYALKPVHSPMAGPIRAVAITVPLVVISAF 302  
 QY 328 ATLFTVNCRKQOENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYCSKQCGQHMY 387  
 Db 303 ATLFTVNCRKQOENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYCSKQCGQHMY 362  
 QY 388 VOCFAYFLQDFCGCEVALDIWEDFSLCREGQREWVTKIHESQFIIVVCSKGMKIFVDKK 447  
 Db 363 VOCFAYFLQDFCGCEVALDIWEDFSLCREGQREWVTKIHESQFIIVVCSKGMKIFVDKK 422  
 QY 448 NYKHGGGGRSGKGLFVAVSAIAEKLRQAKQSSSAALSKEFIIVFYSCGDVPGILD 507  
 Db 423 NYKHGGGGRSGKGLFVAVSAIAEKLRQAKQSSSAALSKEFIIVFYSCGDVPGILD 482  
 QY 508 LSTKYLMDNLPCLSHLSDRGLEQPCQHTROGSRNRYFRSKGSRSLYVAICNMHQFI 567  
 Db 483 LSTKYLMDNLPCLSHLSDRGLEQPCQHTROGSRNRYFRSKGSRSLYVAICNMHQFI 542  
 QY 568 DEEPDWFKEQFVPPHPPPLRYREPVLKEDSLVNDVNCPCGPEDECLKVAEAVLGAT 627  
 Db 543 DEEPDWFKEQFVPPHPPPLRYREPVLKEDSLVNDVNCPCGPEDECLKVAEAVLGAT 602  
 QY 628 GPADSOHESQHGGLDQDGEARPALDGSAAALQPLHHTVKAGSPDMRPSGSIYDSSVPSSE 687  
 Db 603 GPADSOHESQHGGLDQDGEARPALDGSAAALQPLHHTVKAGSPDMRPSGSIYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDQETSSLSVESSSSGLGEERPPALPSKLLSSGCKADLCGRSYTDEL 747  
 Db 663 LSLPLMEGLSTDQETSSLSVESSSSGLGEERPPALPSKLLSSGCKADLCGRSYTDEL 722  
 QY 748 HAVAPL 753  
 Db 723 HAVAPL 728

## RESULT 8

US-09-747-259-18  
 ; Sequence 18, Application US/09747259  
 ; Publication No. US20030008815A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Ranzhong  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: VanLookeren, Menno  
 ; APPLICANT: Vandlen, Richard  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Yansura, Daniel  
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C1P1(US)  
 ; CURRENT APPLICATION NUMBER: US/09/747.259  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: US 09/311,832  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/172,096  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: PCT/US99/31274  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: US 60/175,481  
 ; PRIOR FILING DATE: 2000-01-11  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341  
 ; PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/213,087  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 9; Length 728;  
Best Local Similarity 96.7%; Pred. No. 2.9e-307;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMATAARPLCVANE-GVGPASRNSGLNITFKYDNCNTTLYNPVGRHVIAQAQNTISQY 100  
DB 3 RASAGVPALFVSGGQVGPASRNSGLNITFKYDNCNTTLYNPVGRHVIAQAQNTISQY 62  
QY 101 ACHDQVAVTILWSGALGIEFLKGFVILELKGSGQCOOLILKDPKOLNSSEKFRGTME 160  
DB 63 ACHDQVAVTILWSGALGIEFLKGFVILELKGSGQCOOLILKDPKOLNSSEKFRGTME 122  
QY 161 SQFLANKEFTDYFKVVPVPSIKNESNYHFFETTRACDLILQPDNLACKPFWKPNLN 220  
DB 123 SQFLANKEFTDYFKVVPVPSIKNESNYHFFETTRACDLILQPDNLACKPFWKPNLN 182  
QY 221 ISO-----HGSDMOVSFDHAPHNGPFRFYLYLKLHKGFPKRTCKQOFT 267  
DB 183 ISGSGDAQVSFDHAPHNGPFRFYLYLKLHKGFPKRTCKQOFT 242  
QY 268 ETTSCLLQVSPGYIIELVDDNTTRKVMYALKPVHSPWAGPTRAIVTVPLVLSAF 327  
DB 243 EMTSCLLQVSPGYIIELVDDNTTRKVMYALKPVHSPWAGPTRAIVTVPLVLSAF 302  
QY 328 ATLFTVACRKKQENIYSHLDESSSESTYTAALPRRLRPRPKVFLCYSSKQGNHNV 387  
DB 303 ATLFTVACRKKQENIYSHLDESSSESTYTAALPRRLRPRPKVFLCYSSKQGNHNV 362  
QY 388 VQCFAYFLQDGCCEVALDWEFSLCREGQENVIQIHESQFIVVCSKGMKFDYDKK 447  
DB 363 VQCFAYFLQDGCCEVALDWEFSLCREGQENVIQIHESQFIVVCSKGMKFDYDKK 422  
QY 448 NYKHGGGSGKGLFLVAVSAIAEKLRQAKSSAALSKEFTAVFYDCEGVDPGLD 507  
DB 423 NYKHGGGSGKGLFLVAVSAIAEKLRQAKSSAALSKEFTAVFYDCEGVDPGLD 482  
QY 508 LSTKYRLMDNLPQLCSHLHSDRGHQEPQHTQGRSRRNFRSKGSRSLYVAICNMHOFT 567  
DB 483 LSTKYRLMDNLPQLCSHLHSDRGHQEPQHTQGRSRRNFRSKGSRSLYVAICNMHOFT 542  
QY 568 DEPDWFEKQVPPHPPPLRYEPVLEKFDGSLVNDVCKPQPSDFCLKVAEAVLGAT 627  
DB 543 DEPDWFEKQVPPHPPPLRYEPVLEKFDGSLVNDVCKPQPSDFCLKVAEAVLGAT 602

QY 628 GPADSHQSGHGLDQGEARPALDGSAAALQPLHVTYKAGSPDMPROSGIYDSSVPSSE 687  
DB 603 GPADSHQSGHGLDQGEARPALDGSAAALQPLHVTYKAGSPDMPROSGIYDSSVPSSE 662  
QY 688 LSLPLMEGLSTDOTETSSLTESVSSSGGLGEEPPALPKLLSSGSCRADIGCRSTYDEL 747  
DB 663 LSLPLMEGLSTDOTETSSLTESVSSSGGLGEEPPALPKLLSSGSCRADIGCRSTYDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

## RESULT 9

US-09-908-827-18. Application US/09908827  
Sequence 18, Publication No. US2003003442A1

## GENERAL INFORMATION:

APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tumas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandien, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
TITLE REFERENCE: P138IRIC1C1(US)  
CURRENT APPLICATION NUMBER: US/09/908,827  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816,744

; PRIOR FILING DATE: 2001-03-22  
 ; PRIOR APPLICATION NUMBER: 09/854,208  
 ; PRIOR FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: 09/854,280  
 ; PRIOR FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: PCT/US99/05028  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/10733  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: PCT/US99/31274  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341  
 ; PRIOR FILING DATE: 2000-02-18  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05601  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07532  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264  
 ; PRIOR FILING DATE: 2000-06-02  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: PCT/US00/30873  
 ; PRIOR FILING DATE: 2000-11-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SEQ ID NO 18  
 ; LENGTH: 728  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-09-908-827-18

Query Match 92.38; Score 3703; DB 9; Length 728;  
 Best Local Similarity 96.74; Pred. No. 2.9e-307;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKAAAPRLCVANE-GVGPASRNSGLYNITFKYDNCNTYVLPVKGHVIAADQAQNTISQY 100  
 DB 3 RASAGVPALFVSGGCGVGPASRNSGLYNITFKYDNCNTYVLPVKGHVIAADQAQNTISQY 62  
 QY 101 ACHDOVAVTILASPGALGIEFLKGFVRIEELKSEGRQCOQLILKDPKOLNSSEFKRTGME 160  
 DB 63 ACHDOVAVTILASPGALGIEFLKGFVRIEELKSEGRQCOQLILKDPKOLNSSEFKRTGME 122  
 QY 161 SPPFLNKKFTDYFKVYVPPSPKNSNHYHPPFTRACDLLOPDNLACKPFKPKPNLN 220  
 DB 123 SPPFLNKKFTDYFKVYVPPSPKNSNHYHPPFTRACDLLOPDNLACKPFKPKPNLN 182  
 QY 221 ISQ-----HSGDMQVSDHAPNFGFRFFYLHYKLKHEGPKFKTKCQOTT 267  
 DB 183 ISQHGSDMQVSDHAPNFGFRFFYLHYKLKHEGPKFKTKCQOTT 242  
 QY 268 ETTSCLLQNVSGDYIIELVDDNTTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAF 327  
 DB 243 ETTSCLLQNVSGDYIIELVDDNTTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAF 302  
 QY 328 ATLFTVMCRKQOENIYSHLDESSSESTYTAALPRRLPRPKVFLCYSSKDGONHNV 387  
 DB 303 ATLFTVMCRKQOENIYSHLDESSSESTYTAALPRRLPRPKVFLCYSSKDGONHNV 362  
 QY 388 VQCFAYFLQDFCGCEVALDLWEDFSLCRCQREWVIOKHESQIILVWCSEKMFYVDKK 447  
 DB 363 VQCFAYFLQDFCGCEVALDLWEDFSLCRCQREWVIOKHESQIILVWCSEKMFYVDKK 422  
 QY 448 NTKHKGGRSGKGEFLFVAVSAIAEKLROAKQSSAALSFTAVTFDYSCGDVPGTLD 507  
 DB 423 NTKHKGGRSGKGEFLFVAVSAIAEKLROAKQSSAALSFTAVTFDYSCGDVPGTLD 482

QY 508 LSKYRLMDNLPLCLSHLSRDGLQSPQHTROGSRNRYFRSKSGRSLYVAICNMHOFI 567  
 DB 483 LSKYRLMDNLPLCLSHLSRDGLQSPQHTROGSRNRYFRSKSGRSLYVAICNMHOFI 542  
 QY 568 DEEPDFEKFQVFPFPPPLRYREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAAVLGAT 627  
 DB 543 DEEPDFEKFQVFPFPPPLRYREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAAVLGAT 602  
 QY 628 GPADSHQSHGGLDQGEARPALDGSAAALPPLHTVTKAGSPDMPSDGIYDSSVPSSE 687  
 DB 603 GPADSHQSHGGLDQGEARPALDGSAAALPPLHTVTKAGSPDMPSDGIYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDTQETSSLSVESVSSSGGEEPPALPALKLLSSGSKADLCGRSYTDEL 747  
 DB 663 LSLPLMEGLSTDTQETSSLSVESVSSSGGEEPPALPALKLLSSGSKADLCGRSYTDEL 722  
 QY 748 HAVAPG 753  
 DB 723 HAVAPL 728

RESULT 10  
 ; US-09-912-157-12  
 ; Sequence-12, Application US/09912157  
 ; Patent No. US20020165348A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Kuestner, Rolf E.  
 ; APPLICANT: Gao, Zeren  
 ; TITLE OF INVENTION: Human Cytokine Receptor  
 ; FILE REFERENCE: 00-49  
 ; CURRENT APPLICATION NUMBER: US/09/912,157  
 ; CURRENT FILING DATE: 2001-07-23  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 739  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ; US-09-912-157-12

Query Match 84.4%; Score 3387; DB 9; Length 739;  
 Best Local Similarity 85.2%; Pred. No. 2.7e-280;  
 Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;

QY 1 MAPWLQCSVFETVNAQLNGSQLAAVAGSGGRARGADTCGRWMTATPRLCVANEVGP 60  
 DB 1 MAPWLQCSVFETVNAQLNGSQLAAVAGSGGRARGADTCGRWMTATPRLCVANEVGP 46  
 QY 61 ASNSGLYNITFKYDNCNTYVLPVKGHVIAADQAQNTISQYACHDOVAVTILASPGALGI 119  
 DB 47 ASNSGLYNITFKYDNCNTYVLPVKGHVIAADQAQNTISQYACHDOVAVTILASPGALGI 106  
 QY 120 EFLKGRVILEELKSEGRQCOQLILKDPKOLNSSEFKRTGMEOPFLNKKFTDYFKVVP 179  
 DB 107 EFLKGRVILEELKSEGRQCOQLILKDPKOLNSSEFKRTGMEOPFLNKKFTDYFKVVP 166  
 QY 180 FPSIKNESHYHPPFTRACDLLOPDNLACKPFKPKPNLNISQHGSDMQVSDHAPNFG 239  
 DB 167 FPSIKNESHYHPPFTRACDLLOPDNLACKPFKPKPNLNISQHGSDMQVSDHAPNFG 226  
 QY 240 GFRFFYLHYKLKHEGPKFKTKCQOTTETTSCLLQNVSPDYIIELVDDNTTRKVMHY 299  
 DB 227 GFRFFYLHYKLKHEGPKFKTKCQOTTETTSCLLQNVSPDYIIELVDDNTTRKVMHY 286  
 QY 300 ALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 359  
 DB 287 VVKSQVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 346  
 QY 360 ALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 419  
 DB 347 ALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 406

QY 420 ENVIKIHESOFIIVCSGKMYFYDKNKKHGGSGGSGELFLVAVSAIAEKLRAK 479  
 Db 407 ENAIQKIHESOFIIVCSGKMYFYDKNKKHGGSGGSGELFLVAVSAIAEKLRAK 466  
 QY 480 QSSSAALSKFIAYFYDSGCGVGLDLSKYRLMDNLQCLSHLSRDLGLOEP-CQH 538  
 Db 467 QSSSAALSKFIAYFYDSGCGVGLDLSKYRLMDNLQCLSHLSRDLGLOEP-CQH 523  
 QY 539 TRQGRNRYFRSKSGSLVAICNNHOFIDEEPDMFKQFVFPHPPLRYREPVELEKDS 598  
 Db 524 PGHSRRNRYFRSKSGSLVAICNNHOFIDEEPDMFKQFVFPHPPLRYREPVELEKDS 583  
 QY 599 GLVLDVMCKPGSPDCLKVEAVILGATGADSOH--PSOHGGLDGDGEARPAIDGSA 656  
 Db 584 GLVLDVSKPGSPDCLKVEAVILGATGADSOH--PSOHGGLDGDGEARPAIDGSA 643  
 QY 657 LQPLHIVKAGSPDPRDSGIIYSSVPSSELSPLMAGELSTDDOTERTSSLTSSVSSSGL 716  
 Db 644 LQPLHIVKAGSPDPRDSGIIYSSVPSSELSPLMAGELSTDDOTERTSSLTSSVSSSGL 703  
 QY 717 GREEPPALPKLLSSGCKADIGCRSTYDELHVAAPL 753  
 Db 704 GEEDPPLPKLFAAGVSR-ERGHSHSTDELQALAPL 739

## RESULT 11

US-09-809-567-3

Sequence 3, Application US/09809567

Patent No. US20020045213A1

GENERAL INFORMATION:

APPLICANT: Jing, Shuguan

TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

FILE REFERENCE: 01017/36916A

CURRENT APPLICATION NUMBER: US/09/809,567

PRIOR FILING DATE: 2001-03-15

PRIOR FILING DATE: 09/724,460

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 60/189,816

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 810

TYPE: PRT

ORGANISM: Homo sapiens

US-09-809-567-3

Query Match 7.8%; Score 312; DB 10; Length 810;

Best Local Similarity 23.1%; Pred. No. 8.2e-18;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTLNPKVGHVIAQAQNT-----ISQYACHDQ-----VAVTILWS 113  
 Db 49 NCTVKNSTCLDDSWHP-----RNLTPSPKDLQIQLHFAHTQDGLFPVAHIEMT 99  
 QY 114 -PGALGTEFLKGRVILBELKSEGCQQLILKADPKOLNSFKRTGMSOPFLNMKFTD 172  
 Db 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLHHRRWRTFSHFV-VDPOQE 156  
 QY 173 FYVKV--VPPSPKSNESYHFFFRTRACDLQLQDNLACK--PFWKPNRL----- 219  
 Db 157 YEVTVHLKPIPDGDPNHQSKNELVPCDEHARKVTTTPCMSSGSLMDP-NITVETLEAH 215  
 QY 220 -----NISQSGDMQVDFDAPHNFGRFFFLYHLKKEGFPFKRTCKEQBTETT 270  
 Db 216 QLRVSFTLWNESTHYQILTSFPHNENHSCFEHMH-HIPAPRPEEFHQSRNVTLLRLMK 274  
 QY 271 SCLLQNSYSPGDIYIELVDOT--NTTKVMHYALKRVHSPNAGPIRAVATVPLVVISAF 327  
 Db 275 GCRHQVQIQPFSSCLNDLRHSATSCPEMDPTPEPIDYMLWYFETGISILLVG 334  
 QY 328 ATLTVCKRKKQENIYSHLDESESSYTAALPRERLRPP-----KVLFCYSKQDN 383

Db 335 SVILLIVCMTRLAGPGS-----EKYSDDTKYTGCLPAADLIPPLPKPKVWIISA-DHPL 390  
 QY 384 RHNVVOCFATFYQDQFCGEVALDIEDFSLCHREGQREWV-----IQRTHESQFIIVVCSKG 439  
 Db 391 YDVVLVFAQFLITAGTCEVALDLEQATSEAGVNTWVGRQKQWVESNRIIVLCSRG 450  
 QY 440 MKYFVDFKNTKHKGGG-----RSGSGELFLVAVSAIAEKLRAKQSSAALSKEIA 491  
 Db 451 TR-----AKMALLGRGAPVRLRCDHGRKPGVDLFTAMNMILLDFKR-----PACGTVV 501  
 QY 492 VTF-DYSCGDVGIILDLSTKYRLMDNLQCLSHLSRDLGLOEPGQHTROG--SRNRYF 548  
 Db 502 CYFEVSCGDVDPDLFGAARYPLMDRFEV--YFRIOLEKFGQGMHVRVGLSGDNYL 559  
 QY 549 RSKSGRSLYVAICNNHOFIDEEPDMFE-----KQFVPPHPPPLRYREPVELEKDSGL 600  
 Db 560 RSPGGRQLRAALDRFRDMQVRCDFMFECEMLYSADDDAPSLDEEV-FEPLIPP-GTGI 617  
 QY 601 VLNDVMCKPGSPDCLKVEAVILGATGADSOH-----SQHGG 640  
 Db 618 VKRAPLVRE-PGSOACLAIDPLVGEEGGAVAKLEPHLQPRGQAPQPLHIVLAEEGA 676  
 QY 641 LDQDGEARPAIDGSA---ALQ-----PILHTVKAGSPDPRDSGIIYSSVPSSELSLP 691  
 Db 677 LVAAVEPGPLADGAARLALAGEACEACPLGSPGAG-----RNSVLF---LPVDPDSP 727  
 QY 692 LMEGISTDQTEITSSLTSSVSSSGLEGEPPALPKLLSSGCKADIGC 740  
 Db 728 L--GSSTPMASPOLLPEDVR-----EHLEGIMLSLFEQSLSCQNGCC 768

## RESULT 12

US-09-778-971-9

Sequence 9, Application US/09778971

Patent No. US20020102639A1

GENERAL INFORMATION:

APPLICANT: Shaugnessy, John D.

TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby

FILE REFERENCE: D6138

CURRENT APPLICATION NUMBER: US/09/778,971

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/180,374

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 9

LENGTH: 866

TYPE: PRT

ORGANISM: Unknown

FEATURE:

NAME/KEY: peptide

OTHER INFORMATION: IL-17 receptor protein

US-09-778-971-9

Query Match

Best Local Similarity 23.1%; Pred. No. 9.1e-18;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTLNPKVGHVIAQAQNT-----ISQYACHDQ-----VAVTILWS 113  
 Db 49 NCTVKNSTCLDDSWHP-----RNLTPSPKDLQIQLHFAHTQDGLFPVAHIEMT 99  
 QY 114 -PGALGTEFLKGRVILBELKSEGCQQLILKADPKOLNSFKRTGMSOPFLNMKFTD 172  
 Db 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLHHRRWRTFSHFV-VDPOQE 156  
 QY 173 FYVKV--VPPSPKSNESYHFFFRTRACDLQLQDNLACK--PFWKPNRL----- 219  
 Db 157 YEVTVHLKPIPDGDPNHQSKNELVPCDEHARKVTTTPCMSSGSLMDP-NITVETLEAH 215  
 QY 220 -----NISQSGDMQVDFDAPHNFGRFFFLYHLKKEGFPFKRTCKEQBTETT 270  
 Db 216 QLRVSFTLWNESTHYQILTSFPHNENHSCFEHMH-HIPAPRPEEFHQSRNVTLLRLMK 274

QY 271 SCILQVSPGDIIEIIVDOT---NTRVNHAYALKVPSPAGPIRAVALTVPLVVISAF 327  
 Db 275 GCRHVOVQIOPFFSCLNCLRESATVSCPEMDPTPEPIDYVWMLWYTWITIGISILVG 334  
 QY 328 AILFTVCKKQOENIYSHLDESESTYTAALPRERLRPP---KVFCLYSSKDOON 383  
 Db 335 SVILLVCHWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKWIYISA-DHPL 390  
 QY 384 HNNVOCFAIYFLODFCGCEVALDMEFSLCREGOREW---IQKHESQFIIVVCSKG 439  
 Db 391 YDVLKFAOFLFACGTEVALDLEQAISEAGVNTWGRQKQEMVESKIIIVLCRSG 450  
 QY 440 MYFVDKKNYKHKGKGG-----RSGKGELFLVAVSAIAEKLKRAKQSSAALSFKFA 491  
 Db 451 TR---AKWQALLGRGAPVRLRCDHGKPVGDLEFTAAMNMLPDEKR-----PACFGTVV 501  
 QY 492 VYF-DYSCGDVPGIILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROG---SRNVEF 548  
 Db 502 CYFEVSCDGVDPDLFGAAPRYPLMDREFEV--YFRIQDLEMFQGRHVRHVGELSGDNL 559  
 QY 549 RSKSGSLYVAICNMHOFIDEEDPME-----KQVPPHPPPLRYREPVLKEDSGL 600  
 Db 560 RSPGGRLAALDRFDWQVRCDFECENLYSADDDAPSLDEEV-FEPLPLPP-GTGI 617  
 QY 601 VLMVCKPSPESDFCLKVEAAVGLATGAPDSQHE-----SQHGG 640  
 Db 618 VKRAPLVRE-PGSQACLAIDPLVGEAGAAVAKLEPHLOPQOPAPQPLHTLVLAEEGA 676  
 QY 641 LQDGEARPALDGS---ALQ-----PLLHTVKGAGSPDMRDSGIYDSSVSPSELSLP 691  
 Db 677 LVAAVEPCPLADGAANRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGSLTDQTFSSLTSSVSSSGGLEEPPALPSKLLSSGSKADLGC 740  
 Db 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAGGC 768

RESULT 13  
 US-10-033-522-1  
 ; Sequence 1, Application US/10033522  
 ; Patent No. US20020136724A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOHLER, Kendall M.  
 ; TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists  
 ; FILE REFERENCE: 2982-A  
 ; CURRENT APPLICATION NUMBER: US/10/033,522  
 ; CURRENT FILING DATE: 2001-10-18  
 ; PRIOR APPLICATION NUMBER: US 60/241,230  
 ; PRIOR FILING DATE: 2000-10-18  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO. 1  
 ; LENGTH: 866  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-033-522-1

Query Match 7.8%; Score 312; DB 12; Length 866;  
 Best Local Similarity 23.1%; Pred. No. 9.1e-18;  
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NIFKDYDNC---TTLNVPVGHVHTADQNT-----ISQYACHDQ-----VAIVTILMS 113  
 Db 49 NCTVKNSTCLDSDWIHP-----RNLTSSPKQLOIQLHFAHTQOGLFFVALEWT 99  
 QY 114 -PQALGIEFLKGFVILEELKSGROOQILKDPOLANSFKPTGMSQPLMKAFETD 172  
 Db 100 LQTDASILEGALSILVQLNTERLCVR---FEPLSKLRHHRHRRFTFSHFV-VPODQE 156  
 QY 173 YFVKV---VPFSSIKNESNYHFFFTTRACDLLQPDNLACK---PFMKPRNL----- 219  
 Db 157 YEVTVHHLKPIPDGPDGNHQRNKLFLVPOEARMKVTTCKMSSGSLMDP-NITVETLEAH 215

QY 220 -----NISQSGDMQVDFDHAPNFQFRFFYLHVYKLKHEGPFKRKTCQEQOTTET 270  
 Db 216 QLRVSFTLWNESTHYOILLSEFPMENHSCFEHMH-HIPAPRPEEFHORSNVTLRNLK 274  
 QY 271 SCILQVSPGDIIEIIVDOT---NTRVNHAYALKVPSPAGPIRAVALTVPLVVISAF 327  
 Db 275 GCRHVOVQIOPFFSCLNCLRESATVSCPEMDPTPEPIDYVWMLWYTWITIGISILVG 334  
 QY 328 AILFTVCKKQOENIYSHLDESESTYTAALPRERLRPP---KVFCLYSSKDOON 383  
 Db 335 SVILLVCHWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKWIYISA-DHPL 390  
 QY 384 HNNVOCFAIYFLODFCGCEVALDMEFSLCREGOREW---IQKHESQFIIVVCSKG 439  
 Db 391 YDVLKFAOFLFACGTEVALDLEQAISEAGVNTWGRQKQEMVESKIIIVLCRSG 450  
 QY 440 MYFVDKKNYKHKGKGG-----RSGKGELFLVAVSAIAEKLKRAKQSSAALSFKFA 491  
 Db 451 TR---AKWQALLGRGAPVRLRCDHGKPVGDLEFTAAMNMLPDEKR-----PACFGTVV 501  
 QY 492 VYF-DYSCGDVPGIILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROG---SRNVEF 548  
 Db 502 CYFEVSCDGVDPDLFGAAPRYPLMDREFEV--YFRIQDLEMFQGRHVRHVGELSGDNL 559  
 QY 549 RSKSGSLYVAICNMHOFIDEEDPME-----KQVPPHPPPLRYREPVLKEDSGL 600  
 Db 560 RSPGGRLAALDRFDWQVRCDFECENLYSADDDAPSLDEEV-FEPLPLPP-GTGI 617  
 QY 601 VLMVCKPSPESDFCLKVEAAVGLATGAPDSQHE-----SQHGG 640  
 Db 618 VKRAPLVRE-PGSQACLAIDPLVGEAGAAVAKLEPHLOPQOPAPQPLHTLVLAEEGA 676  
 QY 641 LQDGEARPALDGS---ALQ-----PLLHTVKGAGSPDMRDSGIYDSSVSPSELSLP 691  
 Db 677 LVAAVEPCPLADGAANRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGSLTDQTFSSLTSSVSSSGGLEEPPALPSKLLSSGSKADLGC 740  
 Db 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAGGC 768

RESULT 14  
 US-09-874-503-12  
 ; Sequence 12, Application US/09874503  
 ; Patent No. US20020177188A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Hymowitz, Kenneth J.  
 ; APPLICANT: Hillan, Kenneth G.  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: Starovasnik, Melissa A.  
 ; APPLICANT: VanLookeren, Menno  
 ; APPLICANT: Vandien, Richard  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Yasuura, Daniel  
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C13(US)  
 ; CURRENT APPLICATION NUMBER: US/09/874,503  
 ; CURRENT FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/253,646  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/244,072  
 ; PRIOR FILING DATE: 2000-10-26

Prior Application Number: US 60/242,837  
 Prior Filing Date: 2000-10-24  
 Prior Application Number: US 60/175,481  
 Prior Filing Date: 2000-01-11  
 Prior Application Number: US 60/191,007  
 Prior Filing Date: 2000-03-21  
 Prior Application Number: US 60/213,807  
 Prior Filing Date: 2000-06-22  
 Prior Application Number: US 60/172,096  
 Prior Filing Date: 1999-12-23  
 Prior Application Number: US 60/138,387  
 Prior Filing Date: 1999-06-09  
 Prior Application Number: US 60/134,287  
 Prior Filing Date: 1999-05-14  
 Prior Application Number: US 60/131,022  
 Prior Filing Date: 1999-04-26  
 Prior Application Number: US 60/130,232  
 Prior Filing Date: 1999-04-21  
 Prior Application Number: US 60/113,621  
 Prior Filing Date: 1998-12-23  
 Prior Application Number: US 60/085,579  
 Prior Filing Date: 1998-05-15  
 Prior Application Number: US 09/854,208  
 Prior Filing Date: 2001-05-10  
 Prior Application Number: US 09/854,280  
 Prior Filing Date: 2001-05-20  
 Prior Application Number: US 09/816,744  
 Prior Filing Date: 2001-03-22  
 Prior Application Number: US 09/747,259  
 Prior Filing Date: 2000-12-20  
 Prior Application Number: US 09/644,848  
 Prior Filing Date: 2000-08-22  
 Prior Application Number: US 09/380,142  
 Prior Filing Date: 1999-08-25  
 Prior Application Number: US 09/380,138  
 Prior Filing Date: 1999-08-25  
 Prior Application Number: US 09/311,832  
 Prior Filing Date: 1999-05-14  
 Prior Application Number: US PCT/US01/06520  
 Prior Filing Date: 2001-02-28  
 Prior Application Number: US PCT/US00/34956  
 Prior Filing Date: 2000-12-20  
 Prior Application Number: US PCT/US00/32678  
 Prior Filing Date: 2000-12-01  
 Prior Application Number: US PCT/US00/30873  
 Prior Filing Date: 2000-11-10  
 Prior Application Number: US PCT/US00/23328  
 Prior Filing Date: 2000-08-24  
 Prior Application Number: US PCT/US00/15264  
 Prior Filing Date: 2000-06-02  
 Prior Application Number: US PCT/US00/07532  
 Prior Filing Date: 2000-03-21  
 Prior Application Number: US PCT/US00/05841  
 Prior Filing Date: 2000-03-02  
 Prior Application Number: US PCT/US00/05601  
 Prior Filing Date: 2000-03-01  
 Prior Application Number: US PCT/US00/04341  
 Prior Filing Date: 2000-02-18  
 Prior Application Number: US PCT/US99/31274  
 Prior Filing Date: 1999-12-30  
 Prior Application Number: US PCT/US99/10733  
 Prior Filing Date: 1999-05-14  
 Prior Application Number: US PCT/US99/05028  
 Prior Filing Date: 1999-03-08  
 Number of Seq ID Nos: 39  
 Seq ID No 12  
 Length: 502  
 Type: PRT  
 ORGANISM: Homo Sapien.  
 US-09-874-503-12

Query Match 3.4%; Score 135.5; DB 9; Length 502;  
 Best Local Similarity 20.1%; Pred. No. 0.0046;

Matches 76; Conservative 49; Mismatches 141; Indels 113; Caps 14;  
 QY 218 NINISQSGDMQVSF-----DHAPHNFGFRFFYLHYLKHGPPKRTCTC-----261  
 Db 143 NANNEDGFSMSVNFSTPGCLDH-----IMKYR-----KCVKAGSLMDPN 183  
 QY 262 -----KOBQTE-----TTSCLLQNVSPGDYIIELVDDTNTTRKVMHLYALKPVHSPWAGPIR 313  
 Db 184 ITACKNEETVEVNFTHPL-----CNRYMALIQHSTI-----ICFSQVFEPOHQT 231  
 QY 314 AVAITPLVVISAFATL-----FTVCKRKQOENIYSHLDESSSS 355  
 Db 232 RASVIVPTGDSGATVQLTPFPCTGSDCIHKGTVLVC-----PQTGVFPPLDNKSKPG 288  
 QY 356 TYTAAL-----PRELR-----PRPKVLCYSSKDCGONHMN 386  
 Db 289 GFLPLLLLSLVATVTVAGIYLWHRERIKKTSFTTLLPPIKVLVVPSEICFHR-----346  
 QY 387 VVOCFAFYLDPCGCEVALDWEFSLCREGOREWVIOKHESQFIIVCSKGRYFVDR 446  
 Db 347 TICFTFEIQNCRSEVILEKWKKTAEMGPVQWLATQKCAADKVVYVLLSNDVNSVCDG 406  
 QY 447 KNYKHGGGSGKGELEFVAVSAIAEKLRQAKQSSAASKFTIYFYDSCGDPVGI 506  
 Db 407 TCGKSEGPSSENSQ-DLEPLAFNLFCSDLR-----SQHLHKYVVYFREIDTKDYNAL 460  
 QY 507 DLSTKYRLMDNLPQLCSHL 525  
 Db 461 SVCPKYHLMKDATAFCAEL 479

RESULT 15

US-10-000-157-12  
 ; Sequence 12, Application US/10000157  
 ; Publication No. US20020182673A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul L.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Hymowitz, Sarah  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Staroveshnik, Melissa  
 ; APPLICANT: Vanlookeren, Memo  
 ; APPLICANT: Vandlen, Richard  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Yansura, Daniel  
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C1P4(US)  
 ; CURRENT APPLICATION NUMBER: US/10/000,157  
 ; CURRENT FILING DATE: 2001-10-30  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/113621  
 ; PRIOR FILING DATE: 1998-12-23  
 ; PRIOR APPLICATION NUMBER: 60/130232  
 ; PRIOR FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: 60/131022  
 ; PRIOR FILING DATE: 1999-04-26  
 ; PRIOR APPLICATION NUMBER: 60/134287  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: 60/138387  
 ; PRIOR FILING DATE: 1999-06-09  
 ; PRIOR APPLICATION NUMBER: 60/172096  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: 60/175481





GenCore version 5.1.4 ps-4578  
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OM protein: protein search, using sw model

Run on: May 6, 2003, 13:42:46 ; Search time 153 seconds  
(without alignments)  
3173.098 Million cell updates/sec

Title: US-09-912-157-2  
Perfect score: 4013  
Sequence: 1 MAPWLQCSVFTVNAALNG.....CQADGCRSYDELHVAFL 753

Scoring table: BLOSUM62  
Gapop 10.0, Capext 0.5

Searched: 4569144 segs, 644733110 residues  
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main.\*  
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4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
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24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4013	100.0	753	23	US-09-912-157-2
2	4003	99.8	753	23	US-09-912-157-5
3	3925	97.8	739	23	US-09-912-157-8
4	3901	97.2	738	21	US-09-724-460-2
5	3901	97.2	738	22	US-09-809-567-2
6	3901	97.2	738	26	US-10-216-156-2

7	3835.5	95.6	738	22	US-09-863-818A-10	Sequence 10, Appl
8	3708	92.4	728	25	US-10-104-047-3399	Sequence 3399, Ap
9	3703	92.3	728	21	US-09-747-259-18	Sequence 18, Appl
10	3703	92.3	728	22	US-09-816-744-18	Sequence 18, Appl
11	3703	92.3	728	22	US-09-874-503-18	Sequence 18, Appl
12	3703	92.3	728	23	US-09-808-827-18	Sequence 18, Appl
13	3703	92.3	728	23	US-09-808-827A-18	Sequence 18, Appl
14	3703	92.3	728	24	US-10-000-157-18	Sequence 18, Appl
15	3387	84.4	739	24	US-09-912-157-12	Sequence 12, Appl
16	3176	79.1	595	1	PCT-US02-15899-16	Sequence 16, Appl
17	1976	49.2	435	21	US-09-641-377-617	Sequence 617, App
18	1976	49.2	435	21	US-09-758-472-7594	Sequence 7594, Ap
19	1976	49.2	435	26	US-10-235-926-7594	Sequence 7594, Ap
20	312	7.8	810	21	US-09-724-460-3	Sequence 3, Appl
21	312	7.8	810	22	US-09-809-567-3	Sequence 3, Appl
22	312	7.8	810	26	US-10-216-156-3	Sequence 3, Appl
23	312	7.8	866	1	PCT-US97-21451-4	Sequence 4, Appl
24	312	7.8	866	18	US-09-488-728-4	Sequence 4, Appl
25	312	7.8	866	19	US-09-549-679-10	Sequence 10, Appl
26	312	7.8	866	21	US-09-778-971-9	Sequence 9, Appl
27	312	7.8	866	24	US-10-033-522-1	Sequence 1, Appl
28	312	7.8	866	26	US-10-207-655-107	Sequence 107, App
29	306	7.6	864	1	PCT-US97-21451-2	Sequence 2, Appl
30	306	7.6	864	18	US-09-488-728-2	Sequence 2, Appl
31	306	7.6	864	19	US-09-549-679-2	Sequence 2, Appl
32	271.5	6.8	539	21	US-09-723-232-3	Sequence 3, Appl
33	271.5	6.8	539	22	US-09-810-927B-3	Sequence 3, Appl
34	253.5	5.3	284	20	US-09-641-377-618	Sequence 3, Appl
35	232.5	5.3	207	22	US-09-863-818A-19	Sequence 19, Appl
36	232.5	5.3	207	22	US-09-863-818A-20	Sequence 19, Appl
37	139	3.5	453	27	US-60-443-460-815	Sequence 20, Appl
38	135.5	3.4	238	20	US-09-612-601-2	Sequence 815, App
39	135.5	3.4	385	18	US-09-469-099-106	Sequence 2, Appl
40	135.5	3.4	385	19	US-09-599-3608-106	Sequence 106, App
41	135.5	3.4	385	21	US-09-723-232-7	Sequence 7, Appl
42	135.5	3.4	385	22	US-09-810-927B-7	Sequence 7, Appl
43	135.5	3.4	476	16	US-09-266-406-31	Sequence 31, Appl
44	135.5	3.4	485	16	US-09-266-406-12	Sequence 12, Appl
45	135.5	3.4	488	16	US-09-266-406-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-09-912-157-2  
; Sequence 2, Application US/09912157  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Kuestner, Rolf E.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: Human Cytokine Receptor  
; FILE REFERENCE: 00-49  
; CURRENT APPLICATION NUMBER: US/09/912,157  
; CURRENT FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 753  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-912-157-2

Query Match 100.0%; Score 4013; DB 23; Length 753;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWLQCSVFTVNAALNGSOLAAGSGRAGADTCGRMKAAARPRCLVANEVGP 60  
DB 1 MAPWLQCSVFTVNAALNGSOLAAGSGRAGADTCGRMKAAARPRCLVANEVGP 60  
QY 61 ASRNLNITFKVDKNTYINPVGHVIAQAQNTISQYACHDOVAVTILASGALGIE 120

Db 61 ASRNSGLNITFKYDNCITTYLNPVKHVIADQNTISQYACHQDQAVTILSPGALGTE 120  
 QY 121 FLKGRVILEELKSEGRQCOQILKDPKQNSFKRTGMSQPELNNKFTDYFKVYVFF 180  
 Db 121 FLKGRVILEELKSEGRQCOQILKDPKQNSFKRTGMSQPELNNKFTDYFKVYVFF 180  
 QY 181 PSIKESNYHPPFRACDLOLLQDNLACKPFWKPRNLTISQSGDMQVSDPHAPHNG 240  
 Db 181 PSIKESNYHPPFRACDLOLLQDNLACKPFWKPRNLTISQSGDMQVSDPHAPHNG 240  
 QY 241 FRFFLYLKLHKGPFRTCKQBTETTSCLLQNSVSPGYIIELVDDTNTTRKVMHYA 300  
 Db 241 FRFFLYLKLHKGPFRTCKQBTETTSCLLQNSVSPGYIIELVDDTNTTRKVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQCOENYSHLDESSSSTYTA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQCOENYSHLDESSSSTYTA 360  
 QY 361 LPRERLRPRKPVFLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDIWEDFSLCREGORE 420  
 Db 361 LPRERLRPRKPVFLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDIWEDFSLCREGORE 420  
 QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLQAKQ 480  
 Db 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLQAKQ 480  
 QY 481 SSSAALSKEFTAVFDYSCBQDVPGLDLSKYRLMDNLPOLCSHLHSDRGLOEPCQHT 540  
 Db 481 SSSAALSKEFTAVFDYSCBQDVPGLDLSKYRLMDNLPOLCSHLHSDRGLOEPCQHT 540  
 QY 541 QGSRNNTFRSKGSRSLYVAICNMHQFIDEPDWFKEQFVPPHPPPLAYREPVLKFDGSL 600  
 Db 541 QGSRNNTFRSKGSRSLYVAICNMHQFIDEPDWFKEQFVPPHPPPLAYREPVLKFDGSL 600  
 QY 601 VLNDVCKPGPESDFCLKVEAAVLGATGPADSGHSGHGLDQGEARPALDGSAALOPL 660  
 Db 601 VLNDVCKPGPESDFCLKVEAAVLGATGPADSGHSGHGLDQGEARPALDGSAALOPL 660  
 QY 661 LHTYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLTSSVSSSGLGEE 720  
 Db 661 LHTYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLTSSVSSSGLGEE 720  
 QY 721 PPALPSKLLSSGCKADLCRSYTDHHAVALP 753  
 Db 721 PPALPSKLLSSGCKADLCRSYTDHHAVALP 753

## RESULT 2

US-09-912-157-5

; Sequence 5, Application US/09912157

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-912-157-5

Query Match

Best Local Similarity 99.78; Score 4003; DB 23; Length 753;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPWLQICSVFFTVNACLNGSOLAAAGSGGRGARGADTCGWRMKAARPRCLVANEGVGP 60

Db 1 MAPWLQICSVFFTVNACLNGSOLAAAGSGGRGARGADTCGWRMKAARPRCLVANEGVGP 60

QY 61 ASRNSGLNITFKYDNCITTYLNPVKHVIADQNTISQYACHQDQAVTILSPGALGTE 120  
 Db 61 ASRNSGLNITFKYDNCITTYLNPVKHVIADQNTISQYACHQDQAVTILSPGALGTE 120  
 QY 121 FLKGRVILEELKSEGRQCOQILKDPKQNSFKRTGMSQPELNNKFTDYFKVYVFF 180  
 Db 121 FLKGRVILEELKSEGRQCOQILKDPKQNSFKRTGMSQPELNNKFTDYFKVYVFF 180  
 QY 181 PSIKESNYHPPFRACDLOLLQDNLACKPFWKPRNLTISQSGDMQVSDPHAPHNG 240  
 Db 181 PSIKESNYHPPFRACDLOLLQDNLACKPFWKPRNLTISQSGDMQVSDPHAPHNG 240  
 QY 241 FRFFLYLKLHKGPFRTCKQBTETTSCLLQNSVSPGYIIELVDDTNTTRKVMHYA 300  
 Db 241 FRFFLYLKLHKGPFRTCKQBTETTSCLLQNSVSPGYIIELVDDTNTTRKVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQCOENYSHLDESSSSTYTA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQCOENYSHLDESSSSTYTA 360  
 QY 361 LPRERLRPRKPVFLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDIWEDFSLCREGORE 420  
 Db 361 LPRERLRPRKPVFLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDIWEDFSLCREGORE 420  
 QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLQAKQ 480  
 Db 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLQAKQ 480  
 QY 481 SSSAALSKEFTAVFDYSCBQDVPGLDLSKYRLMDNLPOLCSHLHSDRGLOEPCQHT 540  
 Db 481 SSSAALSKEFTAVFDYSCBQDVPGLDLSKYRLMDNLPOLCSHLHSDRGLOEPCQHT 540  
 QY 541 QGSRNNTFRSKGSRSLYVAICNMHQFIDEPDWFKEQFVPPHPPPLAYREPVLKFDGSL 600  
 Db 541 QGSRNNTFRSKGSRSLYVAICNMHQFIDEPDWFKEQFVPPHPPPLAYREPVLKFDGSL 600  
 QY 601 VLNDVCKPGPESDFCLKVEAAVLGATGPADSGHSGHGLDQGEARPALDGSAALOPL 660  
 Db 601 VLNDVCKPGPESDFCLKVEAAVLGATGPADSGHSGHGLDQGEARPALDGSAALOPL 660  
 QY 661 LHTYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLTSSVSSSGLGEE 720  
 Db 661 LHTYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLTSSVSSSGLGEE 720  
 QY 721 PPALPSKLLSSGCKADLCRSYTDHHAVALP 753  
 Db 721 PPALPSKLLSSGCKADLCRSYTDHHAVALP 753

## RESULT 3

US-09-912-157-8

; Sequence 8, Application US/09912157

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 739

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-912-157-8

Query Match

Best Local Similarity 97.88; Score 3925; DB 23; Length 739;

Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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DB 1 MAPMLQLCSVFTVNAACLSQSLAVAGSGRAGADTCGRMKAAARPRICLVANSGVGP 46  
QY 61 ASRNSGLYNITFKYDNCCTTTLNPGKHVIADAQNTISQYACHDOVAVTILWSPGALGIE 120  
DB 47 ASRNSGLYNITFKYDNCCTTTLNPGKHVIADAQNTISQYACHDOVAVTILWSPGALGIE 106  
QY 121 FLKGFVILLEELKSEGRCQCOOLLKDPKQNSSPFKTGESOPFLNMKFETDVFVAVVPE 180  
DB 107 FLKGFVILLEELKSEGRCQCOOLLKDPKQNSSPFKTGESOPFLNMKFETDVFVAVVPE 166  
QY 181 PSIKNESYHFFETTRACDLLOPDNLACFPKPKPRNLNISOHSDMOVSFOHAPHNG 240  
DB 167 PSIKNESYHFFETTRACDLLOPDNLACFPKPKPRNLNISOHSDMOVSFOHAPHNG 226  
QY 241 FRFFYLHYLKLHKGPPFKTKCKOBTETTSCLLQNVSPGDIIELVDDTNTTKYMHYA 300  
DB 227 FRFFYLHYLKLHKGPPFKTKCKOBTETTSCLLQNVSPGDIIELVDDTNTTKYMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 346  
QY 361 LPRERLRPRPKVFLCYSSKDGONHNNVQCFAYELQDFCGCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRPKVFLCYSSKDGONHNNVQCFAYELQDFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGKGLFVAVSAIAEKLRAQK 480  
DB 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGKGLFVAVSAIAEKLRAQK 466  
QY 541 QGSRNRYFRSKGRSLVAICNNHOFIDEEPDMPEKQFVFPFPPPLRYREPVLKEDFDSL 600  
DB 527 QGSRNRYFRSKGRSLVAICNNHOFIDEEPDMPEKQFVFPFPPPLRYREPVLKEDFDSL 586  
QY 601 VLNDVCKPGEPSDFCLKVEAAVLTGATGADQSHESOGGLDQGEARPALDGSAAQLPL 660  
DB 587 VLNDVCKPGEPSDFCLKVEAAVLTGATGADQSHESOGGLDQGEARPALDGSAAQLPL 646  
QY 661 LHTVAGSPDMPDSDGIYDSSVSPSELSLPLMEGLSTDTOTETSSLTESVSSSGLGEE 720  
DB 647 LHTVAGSPDMPDSDGIYDSSVSPSELSLPLMEGLSTDTOTETSSLTESVSSSGLGEE 706

## RESULT 4

US-09-724-460-2

Sequence 2, Application US/09724460  
GENERAL INFORMATION:  
APPLICANT: Jing, Shuqian  
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof  
FILE REFERENCE: 01017/36916  
CURRENT APPLICATION NUMBER: US/09/724,460  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 60/189,816  
PRIOR FILING DATE: 2000-03-16  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 738  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-460-2

Query Watch

97.28; Score 3901; DB 21; Length 738;

Best Local Similarity 97.64; Pred. No. 0;  
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;  
QY 1 MAPMLQLCSVFTVNAACLSQSLAVAGSGRAGADTCGRMKAAARPRICLVANSGVGP 60  
DB 1 MAPMLQLCSVFTVNAACLSQSLAVAGSGRAGADTCGRMKAAARPRICLVANSGVGP 46  
QY 61 ASRNSGLYNITFKYDNCCTTTLNPGKHVIADAQNTISQYACHDOVAVTILWSPGALGIE 120  
DB 47 ASRNSGLYNITFKYDNCCTTTLNPGKHVIADAQNTISQYACHDOVAVTILWSPGALGIE 106  
QY 121 FLKGFVILLEELKSEGRCQCOOLLKDPKQNSSPFKTGESOPFLNMKFETDVFVAVVPE 180  
DB 107 FLKGFVILLEELKSEGRCQCOOLLKDPKQNSSPFKTGESOPFLNMKFETDVFVAVVPE 166  
QY 181 PSIKNESYHFFETTRACDLLOPDNLACFPKPKPRNLNISOHSDMOVSFOHAPHNG 240  
DB 167 PSIKNESYHFFETTRACDLLOPDNLACFPKPKPRNLNISOHSDMOVSFOHAPHNG 226  
QY 241 FRFFYLHYLKLHKGPPFKTKCKOBTETTSCLLQNVSPGDIIELVDDTNTTKYMHYA 300  
DB 227 FRFFYLHYLKLHKGPPFKTKCKOBTETTSCLLQNVSPGDIIELVDDTNTTKYMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 346  
QY 361 LPRERLRPRPKVFLCYSSKDGONHNNVQCFAYELQDFCGCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRPKVFLCYSSKDGONHNNVQCFAYELQDFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGKGLFVAVSAIAEKLRAQK 480  
DB 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGKGLFVAVSAIAEKLRAQK 466  
QY 481 SSSAALSXFAIVFYDSCSDVPGIIDLSTKYLMDNLPLQCLSHLSRHDGLQEPQCHTR 540  
DB 467 SSSAALSXFAIVFYDSCSDVPGIIDLSTKYLMDNLPLQCLSHLSRHDGLQEPQCHTR 526  
QY 541 QGSRNRYFRSKGRSLVAICNNHOFIDEEPDMPEKQFVFPFPPPLRYREPVLKEDFDSL 600  
DB 527 QGSRNRYFRSKGRSLVAICNNHOFIDEEPDMPEKQFVFPFPPPLRYREPVLKEDFDSL 586  
QY 601 VLNDVCKPGEPSDFCLKVEAAVLTGATGADQSHESOGGLDQGEARPALDGSAAQLPL 660  
DB 587 VLNDVCKPGEPSDFCLKVEAAVLTGATGADQSHESOGGLDQGEARPALDGSAAQLPL 646  
QY 661 LHTVAGSPDMPDSDGIYDSSVSPSELSLPLMEGLSTDTOTETSSLTESVSSSGLGEE 720  
DB 647 LHTVAGSPDMPDSDGIYDSSVSPSELSLPLMEGLSTDTOTETSSLTESVSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPV 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAPV 738

## RESULT 5

US-09-809-567-2

Sequence 2, Application US/09809567  
GENERAL INFORMATION:  
APPLICANT: Jing, Shuqian  
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof  
FILE REFERENCE: 01017/36916A  
CURRENT APPLICATION NUMBER: US/09/809,567  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 09/724,460  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 60/189,816  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 739

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-809-567-2

Query Match: 97.2%; Score 3901; DB 22; Length 738;  
Best Local Similarity: 97.6%; Pred. No. 0;  
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPFLQCSVFTTACVACGAGGGRGADTCGRKAAARPRCLVANEQVGP 60  
DB 1 MAPFLQCSVFTTACVACGAGGGRGADTCGRKAAARPRCLVANEQVGP 60  
QY 61 ASRNSGLNITFKYDNCNTTLPVGRKVIADQNTTISQACHDOVAVTILWSPGALGIE 120  
DB 47 ASRNSGLNITFKYDNCNTTLPVGRKVIADQNTTISQACHDOVAVTILWSPGALGIE 106  
QY 121 FLGFRVILEELKSGRCOCOLILKDPKQNSFKRTGMSQFPFLNMFETDVFVYVVF 180  
DB 107 FLGFRVILEELKSGRCOCOLILKDPKQNSFKRTGMSQFPFLNMFETDVFVYVVF 166  
QY 101 PSIKNESNTHPFFTRACOLLQPNLACKPFWKPRNLNISQSGDMQVDFDHPNFQ 240  
DB 167 PSIKNESNTHPFFTRACOLLQPNLACKPFWKPRNLNISQSGDMQVDFDHPNFQ 226  
QY 241 FREYLYHLKHEGPFKRTKQBOETTETTSCLLQNVSPGDIYIELVDOTNTTRKVMHYA 300  
DB 227 FREYLYHLKHEGPFKRTKQBOETTETTSCLLQNVSPGDIYIELVDOTNTTRKVMHYA 286  
QY 301 LKPVHSPMAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESESSSTYTA 360  
DB 287 LKPVHSPMAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESESSSTYTA 346  
QY 421 WYQKTHESQFIIVVCSKGMKYFVKKNYKHGGRSGGKGLFVAVSAIAELKRAQK 480  
DB 407 WYQKTHESQFIIVVCSKGMKYFVKKNYKHGGRSGGKGLFVAVSAIAELKRAQK 466  
QY 481 SSSAALKSFIAVYDYSCGDVPGILDSTKYRLMDNLQPCSHLSRDHGLQEPGQHT 540  
DB 467 SSSAALKSFIAVYDYSCGDVPGILDSTKYRLMDNLQPCSHLSRDHGLQEPGQHT 526  
QY 541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPWFKEQFVFPFPPPLRYREPVLKFDGSL 600  
DB 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPWFKEQFVFPFPPPLRYREPVLKFDGSL 586  
QY 601 VLNDVCKPGPESDFCLKVEAVALGATGPADSOHESQGGDGDGEARPDALGSAALQPL 660  
DB 587 VLNDVCKPGPESDFCLKVEAVALGATGPADSOHESQGGDGDGEARPDALGSAALQPL 646  
QY 661 LHTVKAQSPDMRDSGIYDSSVSPSELPLMEGLSTDTTETSSLTSSVSSSGLGEE 720  
DB 647 LHTVKAQSPDMRDSGIYDSSVSPSELPLMEGLSTDTTETSSLTSSVSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKRADIGCRSYTDLHAPV 752  
DB 707 PPALPSKLLSSGCKRADIGCRSYTDLHAPV 738

RESULT 6  
US-10-216-156-2

Sequence 2, Application US/10216156  
GENERAL INFORMATION:  
APPLICANT: Jing Shugan  
TITLE OF INVENTION: 16-17 Receptor, Like Molecules and Uses Thereof  
FILE REFERENCE: 0101736916A  
CURRENT APPLICATION NUMBER: US/10/216,156  
PRIOR FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: US/09/809,567  
PRIOR FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 09/774,460

PRIOR FILING DATE: 2000-11-28;  
PRIOR APPLICATION NUMBER: 60/189,816  
PRIOR FILING DATE: 2000-03-16;  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 2  
LENGTH: 738  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-216-156-2

Query Match: 97.2%; Score 3901; DB 26; Length 738;  
Best Local Similarity: 97.6%; Pred. No. 0;  
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPFLQCSVFTTACVACGAGGGRGADTCGRKAAARPRCLVANEQVGP 60  
DB 1 MAPFLQCSVFTTACVACGAGGGRGADTCGRKAAARPRCLVANEQVGP 60  
QY 61 ASRNSGLNITFKYDNCNTTLPVGRKVIADQNTTISQACHDOVAVTILWSPGALGIE 120  
DB 47 ASRNSGLNITFKYDNCNTTLPVGRKVIADQNTTISQACHDOVAVTILWSPGALGIE 106  
QY 121 FLGFRVILEELKSGRCOCOLILKDPKQNSFKRTGMSQFPFLNMFETDVFVYVVF 180  
DB 107 FLGFRVILEELKSGRCOCOLILKDPKQNSFKRTGMSQFPFLNMFETDVFVYVVF 166  
QY 181 PSIKNESNTHPFFTRACOLLQPNLACKPFWKPRNLNISQSGDMQVDFDHPNFQ 240  
DB 167 PSIKNESNTHPFFTRACOLLQPNLACKPFWKPRNLNISQSGDMQVDFDHPNFQ 226  
QY 241 FREYLYHLKHEGPFKRTKQBOETTETTSCLLQNVSPGDIYIELVDOTNTTRKVMHYA 300  
DB 227 FREYLYHLKHEGPFKRTKQBOETTETTSCLLQNVSPGDIYIELVDOTNTTRKVMHYA 286  
QY 301 LKPVHSPMAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESESSSTYTA 360  
DB 287 LKPVHSPMAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESESSSTYTA 346  
QY 361 LPRERLRPRKPVFLCYSSKQGNHNVVOCFAIFLQDFGCEVALDLMEFSLCREQRE 420  
DB 347 LPRERLRPRKPVFLCYSSKQGNHNVVOCFAIFLQDFGCEVALDLMEFSLCREQRE 406  
QY 421 WYQKTHESQFIIVVCSKGMKYFVKKNYKHGGRSGGKGLFVAVSAIAELKRAQK 480  
DB 407 WYQKTHESQFIIVVCSKGMKYFVKKNYKHGGRSGGKGLFVAVSAIAELKRAQK 466  
QY 481 SSSAALKSFIAVYDYSCGDVPGILDSTKYRLMDNLQPCSHLSRDHGLQEPGQHT 540  
DB 467 SSSAALKSFIAVYDYSCGDVPGILDSTKYRLMDNLQPCSHLSRDHGLQEPGQHT 526  
QY 541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPWFKEQFVFPFPPPLRYREPVLKFDGSL 600  
DB 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPWFKEQFVFPFPPPLRYREPVLKFDGSL 586  
QY 601 VLNDVCKPGPESDFCLKVEAVALGATGPADSOHESQGGDGDGEARPDALGSAALQPL 660  
DB 587 VLNDVCKPGPESDFCLKVEAVALGATGPADSOHESQGGDGDGEARPDALGSAALQPL 646  
QY 661 LHTVKAQSPDMRDSGIYDSSVSPSELPLMEGLSTDTTETSSLTSSVSSSGLGEE 720  
DB 647 LHTVKAQSPDMRDSGIYDSSVSPSELPLMEGLSTDTTETSSLTSSVSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKRADIGCRSYTDLHAPV 752  
DB 707 PPALPSKLLSSGCKRADIGCRSYTDLHAPV 738

RESULT 7  
US-09-863-818A-10  
Sequence 10, Application US/09863818A  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.

```

1 TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
2
3 FILE REFERENCE: DX01170R
4
5 CURRENT APPLICATION NUMBER: US/09/863,818A
6
7 CURRENT FILING DATE: 2001-05-23
8
9 PRIOR APPLICATION NUMBER: US 60/206,862
10
11 PRIOR FILING DATE: 2000-05-24
12
13 NUMBER OF SEQ. ID NOS: 22
14
15 SOFTWARE: PatentIn version 3.1
16
17 SEQ ID NO 10
18
19 LENGTH: 738
20
21 TYPE: PRT
22
23 ORGANISM: Homo sapiens
24
25 FEATURE:
26
27 NAME/KEY: misc_feature
28
29 LOCATION: (18)..(18)
30
31 OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
32
33 NAME/KEY: misc_feature
34
35 LOCATION: (26)..(26)
36
37 OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
38
39 NAME/KEY: misc_feature
40
41 LOCATION: (109)..(109)
42
43 OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
44
45 NAME/KEY: misc_feature
46
47 LOCATION: (120)..(120)
48
49 OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
50
51 NAME/KEY: misc_feature
52
53 LOCATION: (134)..(134)
54
55 OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
56
57 NAME/KEY: misc_feature
58
59 LOCATION: (8)..(8)
60
61 OTHER INFORMATION: unknown amino.
62
63 NAME/KEY: misc_feature
64
65 LOCATION: (144)..(144)
66
67 OTHER INFORMATION: unknown amino
68
69 NAME/KEY: misc_feature
70
71 LOCATION: (170)..(170)
72
73 OTHER INFORMATION: unknown amino
74
75 NAME/KEY: misc_feature
76
77 LOCATION: (194)..(194)
78
79 OTHER INFORMATION: unknown amino
80
81 NAME/KEY: misc_feature
82
83 LOCATION: (442)..(442)
84
85 OTHER INFORMATION: unknown amino
86
87 NAME/KEY: misc_feature
88
89 LOCATION: (475)..(475)
90
91 OTHER INFORMATION: unknown amino
92
93 NAME/KEY: misc_feature
94
95 LOCATION: (519)..(519)
96
97 OTHER INFORMATION: unknown amino
98
99 US-09-863-818A-10

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Query Match .. 95.6%; Score 3835.5; DB 22;; Length.738;  
Best Local Similarity 96.4%; Pred. No. 0;  
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;

QY 1 MAPWQLCSVFTVYNACLSQLAVAAGSSGRARGADTCGRMKAAARPLCVANEGVGP 60  
|||||  
Db 1. MAPWQLCSVFTVYNACLSQLAVAAGSSGRARGADTCN-----XGVGP 46

[illegible]

OY	121	FLKGRVIL	EELKSGROCOOL	IADPKOLNSSFKRTGMSQPLNKKFTDYFKVPWF	180
Dd	107	FLKGRVIL	EELKSGROXOOL	IADPKOXNSSFKRTGMSQPLNKKFTDYFR-LSF	165

181	PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHSQSDMQVSYFDHAPHNG	240
QY		
166	SEIPNESNYHDEFFRTRACDLLQPDNLACKPFWKPRNLNISQHSQSDMQVSYFDHAPHNG	235
Dh		

226	DB	FRFYTHYHLKIHGSPFRKTKCKQOQTETMSCLLQNYSPGDYILIELVDQDWTNTRKVMHYA	285
301	QY	LKPVHSPWAGPIRAVAITVPLVWISAFATFTVCRKKOOENITSHLDEESSESITYAA	360
286	DB	LKPVHSPWAGPIRAVAITVPLVWISAFATFTVCRKKOOENITSHLDEESSESITYAA	345
361	QY	LPRERLRPRKPVFLCYSSKQOENBNVQCFAYFLQDFCCCEVALDMEDFSLCREQORE	420
346	DB	LPRERLRPRKPVFLCYSSKQOENBNVQCFAYFLQDFCCCEVALDMEDFSLCREQORE	405
421	QY	WYIOKTHESQFIIVVCSKGMYKPYDKNNTKHKHGGSGGKGEFLVNAVSAETKLRQAKO	480
406	DB	WYIOKTHESQFIIVVCSKGMYKPYDKNNTKHKHGGSGGKGEFLVNAVSAETKLRQAKO	465
481	QY	SSSAALSKFIAVIFYDCBGDVGPIILDLSKYRLMDMLPOLCSSLHSHRDXGIZQEPQOHTR	540
466	DB	SSSAALSKFIAVIFYDCBGDVGPIILDLSKYRLMDMLPOLCSSLHSHRDXGIZQEPQOHTR	525
541	QY	QCSRRNYFRSKGRSLYVAICNMHQFIDBEPDWFKEQFVFPHPPLRYREPLVEKFDGSL	600
526	DB	QCSRRNYFRSKGRSLYVAICNMHQFIDBEPDWFKEQFVFPHPPLRYREPLVEKFDGSL	585
601	QY	VINDVMCKGPESDFCLKVEAAVLGATGPAUSQSHESQHGSLQDQGEARPALDGSAAQLPL	660
586	DB	VINDVMCKGPESDFCLKVEAAVLGATGPAUSQSHESQHGSLQDQGEARPALDGSAAQLPL	645
661	QY	LHTVKAGSPDMPRODGGIYDSSVPSSLSLPLMHGLSTTDQTTETSLTSVSSSSGCGEBE	720
646	DB	LHTVKAGSPDMPRODGGIYDSSVPSSLSLPLMHGLSTTDQTTETSLTSVSSSSGCGEBE	705
721	QY	PPALPSPKLLSSGCKRADIGRSVYTDSELHAVAPL	753
706	DB	PPALPSPKLLSSGCKRADIGRSVYTDSELHAVAPL	738

```

RESULT 8
US-10-104-047-3399
/ SEQUENCE 3399, Application US/10104047
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3399
/ LENGTH: 728
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-3399

```

Query Match	92.4%	Score 3708;	DB 25;	Length 728;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 696;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;

QY	56	EGVGPA	SRNSGL	NYTF	KYDNC	TYLP	VGK	KHVI	ADAQ	NTIS	OYACH	DOVAV	ILMSPG	115
		:	:	:	:	:	:	:	:	:	:	:	:	
Db	31	OGVGPA	SRNSGL	NYTF	KYDNC	TYLP	VGK	KHVI	ADAQ	NTIS	OYACH	DOVAV	ILMSPG	90

QY	116.	ALGIEFLKGRVILFELKSGROCOOLILKDPKQLNSSPKRTGMESQPFNNMKFTDYFV	175
Db	91	ALGIEFLKGRVILFELKSGROCOOLILKDPKQLNSSPKRTGMESQPFNNMKFTDYFV	150

176. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
177. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
178. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
179. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
180. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
181. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
182. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
183. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
184. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
185. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
186. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
187. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
188. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
189. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
190. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
191. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
192. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
193. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
194. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
195. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
196. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
197. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
198. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
199. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235  
200. KVPFPSIKNESYHPFFETRACOLLQPDNLACKPFWKPRNLNISQHCSDMQVSDHA 235

QY 296 VNHATKPVHSPNAGPIRAVATVPLVVISAFATFTVNCCKKQENIYSHLDESSSS 355  
DB 271 VNHATKPVHSPNAGPIRAVATVPLVVISAFATFTVNCCKKQENIYSHLDESSSS 330  
QY 356 TTTAALPRELPRKPVFLCTSSKQGNHNVVQCFATFADPCGCEVALDWEDFSLCR 415  
DB 331 TTTAALPRELPRKPVFLCTSSKQGNHNVVQCFATFADPCGCEVALDWEDFSLCR 390  
QY 416 EGOREWIKIHESQIIIVVCSKGMKFFVDKKNYKHGGSGKGEFLVAVSAIAEKL 475  
DB 391 EGOREWIKIHESQIIIVVCSKGMKFFVDKKNYKHGGSGKGEFLVAVSAIAEKL 450  
QY 476 ROAKSSAALSFIAVYFDYSCEDVPGLDLSKYRLMDNLPLCCHLSHRDGLQEP 535  
DB 451 ROAKSSAALSFIAVYFDYSCEDVPGLDLSKYRLMDNLPLCCHLSHRDGLQEP 510  
QY 536 GQTRGSRNRYFRSGSLVATCNHOFIDEPDMFEKQFVFPFPPPLRYREPVLK 595  
DB 511 GQTRGSRNRYFRSGSLVATCNHOFIDEPDMFEKQFVFPFPPPLRYREPVLK 570  
QY 596 FDSGLVNDVCKPESDPCFLVAAVIGATCPADSQHESQHGGLDQGEARPAIDGSA 655  
DB 571 FDSGLVNDVCKPESDPCFLVAAVIGATCPADSQHESQHGGLDQGEARPAIDGSA 630  
QY 656 ALQPLHTVYKAGSPDMRDSGIYDSSVPSSELSLPLMEGLSTDTOTTSLSLTSVSSSG 715  
DB 631 ALQPLHTVYKAGSPDMRDSGIYDSSVPSSELSLPLMEGLSTDTOTTSLSLTSVSSSG 690  
QY 716 LGEEPPALP5KLLSGSCADLACRSYTDDELHAPVL 753  
DB 691 LGEEPPALP5KLLSGSCADLACRSYTDDELHAPVL 728

RESULT 9  
US-09-747-259-18  
Sequence 18, Application US/09747259  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Li, Hanzhong  
APPLICANT: Tamas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P1 (US)  
CURRENT APPLICATION NUMBER: US/09/747,259  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/213,087  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 21; Length 728;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RHKAAARPRICVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGRHVIADQNTISQY 100  
DB 3 RASAGVPAFLVSGGVGPASRNSGLYNITFKYDNCTTYLNPVGRHVIADQNTISQY 62  
QY 101 ACHDOVAVTILASPGALGIEFLKGFVRVILEELKSGROCOOLILKOPKOLNSFPKRTGME 160  
DB 63 ACHDOVAVTILASPGALGIEFLKGFVRVILEELKSGROCOOLILKOPKOLNSFPKRTGME 122  
QY 161 SOPFLANKFETDFKVVYVPPFS IKESNTHPFFFTACDLILLOPNLACKFKWPRNLN 220  
DB 123 SOPFLANKFETDFKVVYVPPFS IKESNTHPFFFTACDLILLOPNLACKFKWPRNLN 182  
QY 221 ISQ-----HSGDMQVSFDHAPNFGFFFLHYKLKHEGPFKRTKQBOYT 267  
DB 183 ISQHGSDMQVSFDHAPNFGFFFLHYKLKHEGPFKRTKQBOYT 242  
QY 268 ETTSCLLQNVSPGDYIIELVDOTNTTKVMHATKAPVHSPWAGPIRAVATVPLVVISAF 327  
DB 243 ETTSCLLQNVSPGDYIIELVDOTNTTKVMHATKAPVHSPWAGPIRAVATVPLVVISAF 302  
QY 328 ATLFTVNCCKKQENIYSHLDESSSESTVTAALPRELPRKPVFLCTSSKQGNHNV 387  
DB 303 ATLFTVNCCKKQENIYSHLDESSSESTVTAALPRELPRKPVFLCTSSKQGNHNV 362  
QY 388 VOCFAYFLQDFGCEVALDWEDFSLCROREWIKIHESQIIIVVCSKGMKFFVDK 447  
DB 363 VOCFAYFLQDFGCEVALDWEDFSLCROREWIKIHESQIIIVVCSKGMKFFVDK 422  
QY 448 NYKHGGSGKGEFLVAVSAIAEKLROAKSSAALSKFIATVYFDYSCGDPVGLD 507  
DB 423 NYKHGGSGKGEFLVAVSAIAEKLROAKSSAALSKFIATVYFDYSCGDPVGLD 482  
QY 508 LSTYRLMDNLPLCCHLSHRDGLQEPGQHTROGSRNRYFRSGSLVATCNHOFI 567  
DB 483 LSTYRLMDNLPLCCHLSHRDGLQEPGQHTROGSRNRYFRSGSLVATCNHOFI 542  
QY 568 DEEDPWFKEQFVFPFPPPLRYREPVLKEDSGLVNDVCKPESDPCFLVAAVIGAT 627  
DB 543 DEEDPWFKEQFVFPFPPPLRYREPVLKEDSGLVNDVCKPESDPCFLVAAVIGAT 602  
QY 628 GPADSQHESQHGGLDQGEARPAIDGSAALQPLHTVYKAGSPDMRDSGIYDSSVPSSE 687  
DB 603 GPADSQHESQHGGLDQGEARPAIDGSAALQPLHTVYKAGSPDMRDSGIYDSSVPSSE 662



QY 688 LSLPLMEGLSTDTQTSSTSSVSSGLGEEPPALPSKLLSSGCKADLCRSYTDGL 747  
DB 663 LSLPLMEGLSTDTQTSSTSSVSSGLGEEPPALPSKLLSSGCKADLCRSYTDGL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

RESULT 10  
US-09-816-744-18  
Sequence 18, Application US/09816744  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tamas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P2(US)  
CURRENT APPLICATION NUMBER: US/09/816,744  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-816-744-18

Query Match 92.3%; Score 3703; DB 22; Length 728;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 PKAAARPLCYANE-GVGPASRSGLYNITPKYDNCNTYLNPGKHVIAADQNTISQY 100  
DB 3 RASAGVPALFVSGGQVGPASRSGLYNITPKYDNCNTYLNPGKHVIAADQNTISQY 62  
QY 101 ACHDOVATILSPGALGTEFLKFRVILEELKSGROCOOLILKPKOLNSFKRTGME 160  
DB 63 ACHDOVATILSPGALGTEFLKFRVILEELKSGROCOOLILKPKOLNSFKRTGME 122  
QY 161 SQPLLNKFFDYFKVVPFFSIKESNYHPFFTRACDLILQPNLACKPFWKPRNLN 220  
DB 123 SQPLLNKFFDYFKVVPFFSIKESNYHPFFTRACDLILQPNLACKPFWKPRNLN 182  
QY 221 ISQ-----HGSDMQVDFDHPHNGFRFFYLHVKLKHEGPKRTCKQETT 267  
DB 183 ISQHGSDMQVDFDHPHNGFRFFYLHVKLKHEGPKRTCKQETT 242  
QY 268 ETTSCILQNVSPGDIYIELVDVDTTKRYVMHTALPVPISWAGSIRAVAITPLVVISAF 327  
DB 243 ETTSCILQNVSPGDIYIELVDVDTTKRYVMHTALPVPISWAGSIRAVAITPLVVISAF 302  
QY 328 ATLTVNCRKQOENITSHLDEESSESTYTAALPRRLRPRPRVFLCYSSKDGQNHNV 387  
DB 303 ATLTVNCRKQOENITSHLDEESSESTYTAALPRRLRPRPRVFLCYSSKDGQNHNV 362  
QY 388 VOCAFAYLQDFCCGCEVALDQWEDSLCREGQENWYQIKIHESQPIIVVCSKGMKVFVDKK 447  
DB 363 VOCAFAYLQDFCCGCEVALDQWEDSLCREGQENWYQIKIHESQPIIVVCSKGMKVFVDKK 422

QY 448 NYKKGGRGSGKGLFLVAVSATAEKLROAKQSSAALSXFTIATVFDYSCSGDVPGLD 507  
DB 423 NYKKGGRGSGKGLFLVAVSATAEKLROAKQSSAALSXFTIATVFDYSCSGDVPGLD 482  
QY 508 LSTYRLMDNLPLQALSHLFSRDHGLQPGQHTROGSRNRYPRSKSGRSLYVAICNHOPI 567  
DB 483 LSTYRLMDNLPLQALSHLFSRDHGLQPGQHTROGSRNRYPRSKSGRSLYVAICNHOPI 542  
QY 568 DEEDDFEKGQFVFPHPPLRYRREPVLKFKDGLVNDVMCRPGSDPCLKVEAAVLGAT 627  
DB 543 DEEDDFEKGQFVFPHPPLRYRREPVLKFKDGLVNDVMCRPGSDPCLKVEAAVLGAT 602  
QY 628 GPADSQHESQHGGLDQDGEARPALDGSALQPLLHTVAGSDMPDRDSCGITYDSSVPSSE 687  
DB 603 GPADSQHESQHGGLDQDGEARPALDGSALQPLLHTVAGSDMPDRDSCGITYDSSVPSSE 662  
QY 688 LSLPLMEGLSTDTQTSSTSSVSSGLGEEPPALPSKLLSSGCKADLCRSYTDGL 747  
DB 663 LSLPLMEGLSTDTQTSSTSSVSSGLGEEPPALPSKLLSSGCKADLCRSYTDGL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

RESULT 11  
US-09-874-503-18  
Sequence 18, Application US/09874503  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth  
APPLICANT: Hymowitz, Sarah G.  
APPLICANT: Tamas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-874-503-18



Prior Application Number: 60/172,096  
Prior Filing Date: 1999-12-23  
Prior Application Number: 60/175,481  
Prior Filing Date: 2000-01-11  
Prior Application Number: 60/191,007  
Prior Filing Date: 2000-03-21  
Prior Application Number: 60/213,807  
Prior Filing Date: 2000-06-22  
Prior Application Number: 60/242,837  
Prior Filing Date: 2000-10-24  
Prior Application Number: 60/244,072  
Prior Filing Date: 2000-10-26  
Prior Application Number: 09/311,832  
Prior Filing Date: 1999-05-14  
Prior Application Number: 09/380,138  
Prior Filing Date: 1999-08-25  
Prior Application Number: 09/380,142  
Prior Filing Date: 1999-08-25  
Prior Application Number: 09/644,848  
Prior Filing Date: 2000-08-22  
Prior Application Number: 09/747,259  
Prior Filing Date: 2000-12-20  
Prior Application Number: 09/816,744  
Prior Filing Date: 2001-03-22  
Prior Application Number: 09/854,208  
Prior Filing Date: 2001-05-10  
Prior Application Number: 09/854,280  
Prior Filing Date: 2001-05-10  
Prior Application Number: PCT/US99/05028  
Prior Filing Date: 1999-03-08  
Prior Application Number: PCT/US99/10733  
Prior Filing Date: 1999-05-14  
Prior Application Number: PCT/US99/31274  
Prior Filing Date: 1999-12-30  
Prior Application Number: PCT/US00/04341  
Prior Filing Date: 2000-02-18  
Prior Application Number: PCT/US00/05601  
Prior Filing Date: 2000-03-01  
Prior Application Number: PCT/US00/05841  
Prior Filing Date: 2000-03-02  
Prior Application Number: PCT/US00/07532  
Prior Filing Date: 2000-03-21  
Prior Application Number: PCT/US00/15264  
Prior Filing Date: 2000-06-02  
Prior Application Number: PCT/US00/23328  
Prior Filing Date: 2000-08-24  
Prior Application Number: PCT/US00/30873  
Prior Filing Date: 2000-11-10  
Prior Application Number: PCT/US00/32678  
Prior Filing Date: 2000-12-01  
Prior Application Number: PCT/US00/34956  
Prior Filing Date: 2000-12-20  
Prior Application Number: PCT/US01/06520  
Prior Filing Date: 2001-02-28  
Number of Seq ID Nos: 39  
Seq ID No 18  
Length: 728  
Type: PRT  
Organism: Homo Sapien  
US-09-908-827-18

Query Match 92.3%, Score 3703; DB 23; Length 728;  
Best Local Similarity 96.7%, Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMKAARPLCVANE-GVGPASRNSGLNITFKYDNCITLYNPVGRKVIADQNITISQY 100  
DB 3 RASAGVPALFVSGEGVGPASRNSGLNITFKYDNCITLYNPVGRKVIADQNITISQY 62  
QY 101 ACHQDVAVTILNSPGALGTEFLKGRVILELSEKSGROCCQOLILKDPKQLNSFKRTGNE 160  
DB 63 ACHQDVAVTILNSPGALGTEFLKGRVILELSEKSGROCCQOLILKDPKQLNSFKRTGNE 122

QY 161 SOPPLNMRFEIDFVAVVPPFSIKNESNYHPPFFTRACDLLLLQPDMLACKPFWPRNLN 220  
DB 123 SOPPLNMRFEIDFVAVVPPFSIKNESNYHPPFFTRACDLLLLQPDMLACKPFWPRNLN 182  
QY 221 TSO-----HGSMDQV3FDHAPHNFGREFYLYLTKLKBEGPFRKTKOEQT 267  
DB 183 TSOHGSMDQV3FDHAPHNFGREFYLYLTKLKBEGPFRKTKOEQT 242  
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPNAGPIRAVAITVPLVVISAF 327  
DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPNAGPIRAVAITVPLVVISAF 302  
QY 328 ATLTVWCRKKQOENIYSHLDESESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHV 387  
DB 303 ATLTVWCRKKQOENIYSHLDESESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHV 362  
QY 388 VOCFAFLQDFCCCEVALDMEDFSLCREGQREWYQKHESQFIIVVCSKGMKTFVOKK 447  
DB 363 VOCFAFLQDFCCCEVALDMEDFSLCREGQREWYQKHESQFIIVVCSKGMKTFVOKK 422  
QY 448 NYKHGGGSGKGLFVAVSAIAELRQAKQSSAALSFIAYFYDYSCEGDVPGILD 507  
DB 423 NYKHGGGSGKGLFVAVSAIAELRQAKQSSAALSFIAYFYDYSCEGDVPGILD 482  
QY 508 LSTKYRLMDNLPOLCASHLSRDHGLQBPQGTROGSRNRYFRSKSGSLVAICNHOPI 567  
DB 483 LSTKYRLMDNLPOLCASHLSRDHGLQBPQGTROGSRNRYFRSKSGSLVAICNHOPI 542  
QY 568 DEEDPWEKOFVFFHPPLRYREPVLEKFDGSLVNDVCKPSPESDFCLKVEAVLQAT 627  
DB 543 DEEDPWEKOFVFFHPPLRYREPVLEKFDGSLVNDVCKPSPESDFCLKVEAVLQAT 602  
QY 628 GPASQHESQHGGLDQGEARPAIDGSAALQPLHTYVAGSPDNPRDSGIYDSSVPSE 687  
DB 603 GPASQHESQHGGLDQGEARPAIDGSAALQPLHTYVAGSPDNPRDSGIYDSSVPSE 662  
QY 688 LSLPLMEGLSTDTSTSSITVESVSSSGLGEPEPPALPSPKLSGSGCKADLCGRSYTDEL 747  
DB 663 LSLPLMEGLSTDTSTSSITVESVSSSGLGEPEPPALPSPKLSGSGCKADLCGRSYTDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

## RESULT 13

US-09-908-827A-18  
Sequence 18, Application US/09908827A  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillen, Kenneth  
APPLICANT: VanLooken, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381RIPC1(US)  
CURRENT APPLICATION NUMBER: US/09/908,827A  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113,621  
PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: 60/130,232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131,022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/134,287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/138,387  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: 60/172,096  
 PRIOR FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/175,481  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: 60/191,007  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/213,807  
 PRIOR FILING DATE: 2000-06-22  
 PRIOR APPLICATION NUMBER: 60/242,837  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: 60/244,072  
 PRIOR FILING DATE: 2000-10-26  
 PRIOR APPLICATION NUMBER: 09/311,832  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 09/380,138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380,142  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/644,848  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: 09/747,259  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: 09/816,744  
 PRIOR FILING DATE: 2001-03-22  
 PRIOR APPLICATION NUMBER: 09/854,208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 09/854,280  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: PCT/US99/05028  
 PRIOR FILING DATE: 1999-03-08  
 PRIOR APPLICATION NUMBER: PCT/US99/10733  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: PCT/US99/31274  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: PCT/US00/04341  
 PRIOR FILING DATE: 2000-02-18  
 PRIOR APPLICATION NUMBER: PCT/US00/05601  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: PCT/US00/07532  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: PCT/US00/15264  
 PRIOR FILING DATE: 2000-06-02  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: PCT/US00/30873  
 PRIOR FILING DATE: 2000-11-10  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO 18  
 LENGTH: 728  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-908-827A-18

Query Match 92.34; Score 3703; DB 23; Length 728;  
 Best Local Similarity 96.74; Pred. NO. 0;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKAAARPLCVANE-CVGPASRNSGLNITFYDNCTTILNPVKRVIADAQNTISQY 100  
 DB 3 RASAGVPALEFVSGOGVGPASRNSGLNITFYDNCTTILNPVKRVIADAQNTISQY 62  
 QY 101 ACHDOVAVTILWSPGALGTEFLKGRVILBELSEGRQCOQILILKDPQLNSFKRTGME 160  
 DB 63 ACHDOVAVTILWSPGALGTEFLKGRVILBELSEGRQCOQILILKDPQLNSFKRTGME 122  
 QY 161 SOPFLNNKFETDYFVKVVPFSPISKNESNYHPFFFRACDLLLLQPDNLACKPFWKPRNLN 220  
 DB 123 SOPFLNNKFETDYFVKVVPFSPISKNESNYHPFFFRACDLLLLQPDNLACKPFWKPRNLN 182  
 QY 221 ISQ-----HGSDMOVSPDHAPHNFGFRFFYLHYKLHHEGPPFRKTKCKEQTT 267  
 DB 183 ISQHGSDMOVSPDHAPHNFGFRFFYLHYKLHHEGPPFRKTKCKEQTT 242  
 QY 268 ETSCLLQNSPGDYIELVDYDTNTTKVHYALKPVHSPWAGPIRAVAITVPLVVISAF 327  
 DB 243 ETSCLLQNSPGDYIELVDYDTNTTKVHYALKPVHSPWAGPIRAVAITVPLVVISAF 302  
 QY 328 ATLFTVMCKKQENIYSHLDEESSESTYTAALPRERLRPRKVFCLCYSKGQONHMY 387  
 DB 303 ATLFTVMCKKQENIYSHLDEESSESTYTAALPRERLRPRKVFCLCYSKGQONHMY 362  
 QY 388 VOCFAFYLFQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIYVVCSGKMKYFVDRK 447  
 DB 363 VOCFAFYLFQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIYVVCSGKMKYFVDRK 422  
 QY 448 NYKHKGGRGSGKGLFLVAVSAIAEKLRQAKQSSAALSKEIAYFYDSCGSDVPGLD 507  
 DB 423 NYKHKGGRGSGKGLFLVAVSAIAEKLRQAKQSSAALSKEIAYFYDSCGSDVPGLD 482  
 QY 508 LSTKYFLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 567  
 DB 483 LSTKYFLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 542  
 QY 568 DEEPDWFKEQVPPHPPPPLAYREPVLKFDGSLVINDVMCKPGPESDCLKVEANVLGAT 627  
 DB 543 DEEPDWFKEQVPPHPPPPLAYREPVLKFDGSLVINDVMCKPGPESDCLKVEANVLGAT 602  
 QY 628 GPADSCHESQHGGLDQGEARPALDGSAAALQPLLHTVKGASPSDMPDROGGIYDSSVPSSE 687  
 DB 603 GPADSCHESQHGGLDQGEARPALDGSAAALQPLLHTVKGASPSDMPDROGGIYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDQETTSLSITESVSSSGLGEEPPALPSKLLSSGSKADIGCRSYTDEL 747  
 DB 663 LSLPLMEGLSTDQETTSLSITESVSSSGLGEEPPALPSKLLSSGSKADIGCRSYTDEL 722  
 QY 748 HAVAPL 753  
 DB 723 HAVAPL 728

RESULT 14  
 US-10-000-157-18  
 ; Sequence 18, Application US/10000157  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul L.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Hymowitz, Sarah  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Starovasinik, Melissa  
 ; APPLICANT: Vanlookeren, Menno  
 ; APPLICANT: Vandlen, Richard  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William  
APPLICANT: Yasuura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P4(US)  
CURRENT APPLICATION NUMBER: US/10/000,157  
CURRENT FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/253646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/908827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264

QY 688 LSLPMLGSLDQETSSLTSSVSSSGLGEEPPALPSPKLLSSGCKADLGCGRSYTDEL 747  
 Db 663 LSLPMLGSLDQETSSLTSSVSSSGLGEEPPALPSPKLLSSGCKADLGCGRSYTDEL 722  
 QY 748 HAVAPL 753  
 Db 723 HAVAPL 728

## RESULT 15

US-09-912-157-12

Sequence 12, Application US/09912157

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/09/912,157

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO. 12

LENGTH: 739

TYPE: PRT

ORGANISM: Mouse

US-09-912-157-12

Query Match 84.4% Score 3387; DB 23; Length 739;  
 Best Local Similarity 85.2%; Pred. No. 0;  
 Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;

QY 1 MAPVLQCSFEFTVNAVLGSLQAVAGSGRGAGADTCGWRKAAARPLCVANEGVGP 60  
 Db 1 MAPVLQCSFEFTVNAVLGSLQAVAGSGRGAGADTCGWR-----GVGP 46  
 QY 61 ASRNSGLNITFFKQNTYLP-VGKHVIADQNTISQYACHQDVAVTILMSPGALGI 119  
 Db 47 ASRNSGLNITFRDNTYLPNGGKHAJADQNTISQYACHQDVAVTILMSPGALGI 106  
 QY 120 EFLKGFVILEELKSGROCOOLILKDPKQLNSFKRTGMSQPLANKFETDYFVKVVP 179  
 Db 107 EFLKGFVILEELKSGROCOOLILKDPKQLNSFKRTGMSQPLANKFETDYFVKVVP 166  
 QY 180 FPSIKNESNTHPFFRTRACDLLOPNLACKPFWKPRNLNISQHSQDNQVSDHAPQNF 239  
 Db 167 FPSIKNESNTHPFFRTRACDLLOPNLACKPFWKPRNLNISQHSQDNQVSDHAPQNF 226  
 QY 240 GFRFTYLYLKHGEPKRTCKQOTETTSCLLQNVSPGDYIIELVDDQNTNRYWHY 299  
 Db 227 GFRGPHVLYLKHGEPFRTRCRQONTETTSCLLQNVSPGDYIIELVDDQNTNRYWHY 286  
 QY 300 ALKPVHSPWAGPIRAVAITVPLWISAFATLFTVMCKKQENIYSHLDEESSESTYTA 359  
 Db 287 VVKSQSPWAGPIRAVAITVPLWISAFATLFTVMCKKQENIYSHLDEESSESTYTA 346  
 QY 360 ALPRRLRPRKPVLCYSSKQDNEMNYYQCFAYFLQDFCGCEVALDLWEDFSLCREGOR 419  
 Db 347 ALPRDLRPPQKPVLCYSNKKQDNEMNYYQCFAYFLQDFCGCEVALDLWEDFSLCREGOR 406  
 QY 420 ENWIOKIHESQIIVVCSKGMFYVDKKNYKHGSGRGKGLFLVAVSAIAEKLRQAK 479  
 Db 407 ENAIQKIHESQIIVVCSKGMFYVDKKNYKHGSGRGKGLFLVAVSAIAEKLRQAK 466  
 QY 480 QSSSAALSFTYVDFSCGQVPGILDSTKYKLMQNLPLCLSHLSRQGLQEP-GQH 538  
 Db 467 QSSSAALRFTYVDFSCGQVPCSLDSTKYKLMQNLPLCLSHLSRQGLQEP-GQEVILGH 523  
 QY 539 TROGSRNRYFSKSGSLYVAICNKHQFIDEEDWFEKQFVFPHPPLRYREPVEKFDOS 598  
 Db 524 PGHSSRRNRYFSKSGSLYVAICNKHQFIDEEDWFEKQFIPQHPVRYQEPVEKFDOS 583

QY 599 GLIVLNDVNCERGPESDFCLKVEAAVLTGNTGPAISQH--ESORHGGLDQGEARPALDGSAA 656  
 Db 584 GLIVLNDVIRGPGESDFCKRVEACVIGAGPADISTYLESORHVGLDQDTEAQFSCDSAPA 643  
 QY 657 LQPLLRVTKAGSPDMPKDSGIYDSVSPSELSLPLMEGLSTDQETSSLTSSVSSSGL 716  
 Db 644 LQPLLRVTKAGSPDMPKDSGIYDSVSPSELSLPLMEGLSTDQETSSLTSSVSSSGL 703  
 QY 717 GDEEPPALPSPKLLSSGCKADLGCGRSYTDELHAVAPL 753  
 Db 704 GDEEPPALPSPKLLSSGCKADLGCGRSYTDELHAVAPL 739

Search completed: May 16, 2003, 13:48:57  
 Job time: 158 secs